

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 6, 2003, 07:33:45 ; Search time 1640.18 Seconds
(without alignments)
108.616 Million cell updates/sec

Title: US-09-540-843-9
Perfect score: 11
Sequence: 1 ctaacctaac 11

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 60474

Minimum DB seq length: 0
Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estm:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pin:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	11	100.0	19	17	AZ614760 1M0443A17
C 2	11	100.0	20	17	AL472050 T. brucei
C 3	11	100.0	25	17	AL462065 T. brucei
C 4	11	100.0	27	17	AZ803795 2M0009M20
C 5	11	100.0	40	17	AZ380089 1M0135K14
C 6	9.4	85.5	22	17	AZ666649 1M0548M19

7	9.4	85.5	29	17	AZ514597
8	9.4	85.5	33	12	BG419809
9	9.4	85.5	33	17	AZ334282 1M0063B08
10	9.4	85.5	34	17	AZ776073 2M0009M20
11	9.4	85.5	36	17	AL767851 Arabidops
12	9.4	85.5	39	9	AU008671
13	9	81.8	22	14	D18745
14	9	81.8	31	17	AL756692
15	9	81.8	32	9	AU255689
16	9	81.8	33	17	BH862417
17	9	81.8	34	17	AZ643251 1M0506F04
18	9	81.8	36	17	BH789800
19	9	81.8	40	9	AI507758
20	9	81.8	40	14	WI2126
21	8.4	76.4	21	17	AZ766315
22	8.4	76.4	23	17	TA319C11P
23	8.4	76.4	24	9	AU256889
24	8.4	76.4	25	10	AV544203
25	8.4	76.4	25	17	TA274G11Q
26	8.4	76.4	27	9	AU255344
27	8.4	76.4	27	14	L32043
28	8.4	76.4	27	17	AZ789654
29	8.4	76.4	30	10	BE385567
30	8.4	76.4	30	17	AZ761166
31	8.4	76.4	31	10	BE409249
32	8.4	76.4	31	13	BM017239
33	8.4	76.4	31	17	AZ782241
34	8.4	76.4	32	12	BE901763
35	8.4	76.4	32	17	AL766020
36	8.4	76.4	32	17	AZ591773
37	8.4	76.4	33	17	AZ591773
38	8.4	76.4	34	9	AI047833
39	8.4	76.4	34	9	AI132658
40	8.4	76.4	34	12	BE729288
41	8.4	76.4	34	13	BI913027
42	8.4	76.4	34	17	TA293C07Q
43	8.4	76.4	35	9	AU263853
44	8.4	76.4	35	17	AZ389531
45	8.4	76.4	36	14	R77023

ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION
19 bp DNA linear GSS 13-DEC-2000
1M0443A17R Mouse 10kb plasmid UUG1M library Mus musculus genomic
clone UUG1M0443A17 R, DNA sequence.
ACCESSION
AZ614760
VERSION
GSS.
KEYWORDS
SOURCE
house mouse.
ORGANISM
Mus musculus
REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
Plasmid inserts
JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

Plate: 0443 row: A column: 17		Barrell, Oxford University Press, 1999).	
Seq primer: CACACGAGAAACGCTATGACC		Email: nelsayed@tigr.org	
Class: plasmid ends		Details of T. brucei sequencing at the Sanger Centre are available	
High quality sequence stop: 19.		at http://www.sanger.ac.uk/Projects/T_brucei/ .	
FEATURES	Location/Qualifiers	Location/Qualifiers	
	1..19	1..20	
source	/organism="Mus musculus"	/organism="Trypanosoma brucei"	
	/strain="C57BL/6J"	/strain="TREU927"	
	/db_xref="taxon:10090"	/db_xref="taxon:5691"	
	/clone="UUGC1M0443A17"	/clone="158a03"	
	/clone_lib="Mouse 10kb plasmid UUGC1M library"	6 a 11 c 0 g 3 t	
	/sex="Male"		
	/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"		
	/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource		
	(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114[gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."		
BASE COUNT	3 a 0 c 10 g 6 t		
	ORIGIN		
Query Match	100.0%; Score 11; DB 17; Length 19;		
	Best Local Similarity 100.0%; Pred. No. 7.1e+03;		
Matches	11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 CTAACCCCTAAC 11	1 CTAACCCCTAAC 11	
Db	19 CTAACCCCTAAC 9	4 CTAACCCCTAAC 14	
RESULT 2			
	TA158A03P	TA84A06P	
LOCUS	20 bp DNA linear GSS 13-DEC-2000	25 bp DNA linear GSS 13-DEC-2000	
	T. brucei sheared genomic DNA clone 158a03, forward sequence, genomic survey sequence.	T. brucei sheared genomic DNA clone 84a06, forward sequence, genomic survey sequence.	
ACCESSION	AL472050	AL462065	
	AL472050.1 GI:11837404	AL462065.1 GI:11860923	
KEYWORDS	GSS.	GSS.	
	Trypanosoma brucei.	Trypanosoma brucei.	
SOURCE	Trypanosoma brucei	Trypanosoma brucei	
	Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.	Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.	
REFERENCE	1 (bases 1 to 20)	1 (bases 1 to 25)	
	Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G.	Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G.	
TITLE	Direct Submission	Direct Submission	
	Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk	Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk	
COMMENT	Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).	Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).	
Email: nelsayed@tigr.org		Email: nelsayed@tigr.org	
	Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/ .	Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/ .	
FEATURES	Location/Qualifiers	Location/Qualifiers	
	1..25	1..25	
source	/organism="Trypanosoma brucei"	/organism="Trypanosoma brucei"	
	/strain="TREU927"	/strain="TREU927"	
	/db_xref="taxon:5691"	/db_xref="taxon:5691"	
	/clone="84a06"	/clone="84a06"	
BASE COUNT	4 a 0 c 12 g 9 t	4 a 0 c 12 g 9 t	
	ORIGIN		
Query Match	100.0%; Score 11; DB 17; Length 25;		
	Best Local Similarity 100.0%; Pred. No. 7.8e+03;		
Matches	11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 CTAACCCCTAAC 11	1 CTAACCCCTAAC 11	
Db	22 CTAACCCCTAAC 12		

RESULT 4

AZ803795
 LOCUS 27 bp DNA linear GSS 16-FEB-2001
 DEFINITION 2M064D22F Mouse 10kb plasmid UUGCLM library Mus musculus genomic
 clone UUGC2M0064D22 F, DNA sequence.
 ACCESSION AZ803795
 VERSION AZ803795.1 GI:12956118
 KEYWORDS GSS..
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 27)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
 M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
 and Wright,D., Weiss,R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0064 row: D column: 22
 Seq primer: CGTTGTAACAGCAGCCAGT
 Class: plasmid ends
 High quality sequence stop: 27.
 FEATURES
 Location/Qualifiers
 1..27
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0064D22"
 /clone_lib="Mouse 10kb plasmid UUGCLM library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adapted DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi14732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adapted mouse DNA was annealed to
 adapted vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT
 ORIGIN

Query Match 100.0%; Score 11; DB 17; Length 27;
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTAACCCCTAAC 11
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 DB 10 CTAACCCCTAAC 20

RESULT 5

AZ380089
 LOCUS 40 bp DNA linear GSS 02-OCT-2000
 DEFINITION 1M0135K14R Mouse 10kb plasmid UUGCLM library Mus musculus genomic
 clone UUGCLM0135K14 R, DNA sequence.
 ACCESSION AZ380089
 VERSION AZ380089.1 GI:10493789
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 40)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
 M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
 and Wright,D., Weiss,R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0135 row: K column: 14
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 40.
 FEATURES
 Location/Qualifiers
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 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGCLM0135K14"
 /clone_lib="Mouse 10kb plasmid UUGCLM library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adapted DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi14732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adapted mouse DNA was annealed to
 adapted vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT
 ORIGIN

Query Match 100.0%; Score 11; DB 17; Length 40;
 Best Local Similarity 100.0%; Pred. No. 8.9e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTAACCCCTAAC 11
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 DB 2 CTAACCCCTAAC 12

RESULT 6
 AZ666649/c
 LOCUS
 DEFINITION 22 bp DNA linear GSS 14-DEC-2000
 1M0548M19R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0548M19 R, DNA sequence.
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 house mouse.
 Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 22)
 REFERENCE
 AUTHORS
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly
 ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
 and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 JOURNAL
 COMMENT
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0548 row: M column: 19
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 22.
 Location/Qualifiers

FEATURES

1..22

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0548M19"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (gi14732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

BASE COUNT 3 a 0 c 14 g 5 t

ORIGIN

Query Match 85.5%; Score 9.4; DB 17; Length 22;
 Best Local Similarity 90.9%; Pred. No. 6.9e+04;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTAACCCCTAAC 11

||| |||||

Db 14 CTACCCCTAAC 4

RESULT 7

AZ514597

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Robert B. Weiss

University of Utah

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0361 row: E column: 14

Seq primer: CGTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 29.

Location/Qualifiers

1..29

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/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0361E14"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (gi14732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

BASE COUNT 6 a 9 c 6 g 8 t

ORIGIN

Query Match 85.5%; Score 9.4; DB 17; Length 29;
 Best Local Similarity 90.9%; Pred. No. 7.5e+04;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTAACCCCTAAC 11

|||||

Db 2 CTAACCCCTAAC 12

AZ514597
 1M0361E14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0361E14 F, DNA sequence.
 AZ514597
 AZ514597.1 GI:10695829
 GSS.
 house mouse.
 Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 29)
 REFERENCE
 AUTHORS
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly
 ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
 and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 JOURNAL
 COMMENT
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0361 row: E column: 14
 Seq primer: CGTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 29.
 Location/Qualifiers

FEATURES

1..29

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0361E14"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

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(http://www.jax.org/resources/documents/dnares/). The DNA

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polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (gi14732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

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chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."


```

RESULT 8
BG419809/c
LOCUS
DEFINITION
  BG419809
  602453261f1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:4591599 5',
  mRNA sequence.
ACCESSION
  BG419809
VERSION
  BG419809.1 GI:13326315
KEYWORDS
  EST.
SOURCE
  human.
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 33)
  NIH-MGC http://mgc.nci.nih.gov/.
  National Institutes of Health, Mammalian Gene Collection (MGC)
  Unpublished (1999)
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/BTP
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLC1328 row: j column: 16
High quality sequence stop: 33.
FEATURES
  Location/Qualifiers
    1..33
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /clone="IMAGE:4591599"
    /clone_lib="NIH_MGC_14"
    /tissue_type="renal cell adenocarcinoma"
    /lab_host="DH10B (phage-resistant)"
    /note="Organ: kidney; Vector: pOT7; Site_1: XhoI; Site_2:
    EcoRI; cDNA made by oligo-dT priming. Directionally
    cloned into EcoRI/XhoI sites using the following 5'
    adaptor: GGCACGAG(G). Size-selected >500bp for average
    insert size 1.8kb. Library constructed by Ling Hong in
    the laboratory of Gerald M. Rubin (University of
    California, Berkeley) using ZAP-cDNA synthesis kit
    (Stratagene) and Superscript II RT (Life Technologies)."
```

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BASE COUNT      9 a      3 c      12 g      9 t
ORIGIN
  Query Match      85.5%; Score 9.4; DB 12; Length 33;
  Best Local Similarity 90.9%; Pred. No. 7.8e+04;
  Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY      1 CTAACCCCTAAC 11
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        17 CTCACCCCTAC 7
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RESULT 9
AZ334282
LOCUS
DEFINITION
  AZ334282
  1M0063B08R Mouse 10kb plasmid UUGCLM library Mus musculus genomic
  clone UUGCLM0063B08 R, DNA sequence.
ACCESSION
  AZ334282
VERSION
  AZ334282.1 GI:10401456
KEYWORDS
  GSS.
SOURCE
  house mouse.
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  1 (bases 1 to 33)
REFERENCE
  1 (bases 1 to 33)
  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
  Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly
  ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
  and Wright,D.,Weiss,R.
  Mouse whole genome scaffolding with paired end reads from 10kb
```

```

plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0063 row: B column: 08
Seq primer: CACACAGAAACACGCTATGACC
Class: plasmid ends
High quality sequence stop: 33.
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  Location/Qualifiers
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    /organism="Mus musculus"
    /strain="C57BL/6J"
    /db_xref="taxon:10090"
    /clone="UUGCLM0063B08"
    /clone_lib="Mouse 10kb plasmid UUGCLM library"
    /sex="Male"
    /lab_host="E. Coli strain XL10-Gold, T1-resistant, P-"
    /note="Vector: PWD42nv; Purified genomic DNA from M.
    musculus C57BL/6J (male) was obtained from the Jackson
    Laboratory Mouse DNA Resource
    (http://www.jax.org/resources/documents/dnares/). The DNA
    was hydrodynamically sheared by repeated passage through a
    0.005 inch orifice at constant velocity. The sheared DNA
    was blunt end-repaired with T4 DNA polymerase and T4
    polynucleotide kinase. Adaptor oligonucleotides were
    ligated to the blunt ends in high molar excess. The
    adapted DNA was purified and size-selected for a 9.5 to
    10.5 kb range using preparative agarose gel
    electrophoresis. Vector DNA was prepared from a derivative
    of pWD42 (gll47321141gb/AF129072.1), a copy-number
    inducible derivative of plasmid R1. The vector was ligated
    with adaptors complementary to the insert adaptors and
    purified. The sheared, adapted mouse DNA was annealed to
    chemically-competent E. coli XL10-Gold (Stratagene) cells
    and selected for ampicillin resistance."
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```

BASE COUNT      11 a      13 c      2 g      7 t
ORIGIN
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  Query Match      85.5%; Score 9.4; DB 17; Length 33;
  Best Local Similarity 90.9%; Pred. No. 7.8e+04;
  Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY      1 CTAACCCCTAAC 11
        |||
        12 CTAACCCCTAAC 22
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RESULT 10
AZ776073
LOCUS
DEFINITION
  AZ776073
  2M0009M20F Mouse 10kb plasmid UUGCLM library Mus musculus genomic
  clone UUGC2M0009M20 F, DNA sequence.
ACCESSION
  AZ776073
VERSION
  AZ776073.1 GI:12903271
KEYWORDS
  GSS.
SOURCE
  house mouse.
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  1 (bases 1 to 34)
REFERENCE
  1 (bases 1 to 34)
  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
  Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly
  ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
  and Wright,D.,Weiss,R.
  Mouse whole genome scaffolding with paired end reads from 10kb
```

```

JOURNAL
COMMENT
    plasmid inserts
    Unpublished (2000)
    Contact: Robert B. Weiss
    University of Utah Genome Center
    University of Utah
    Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLc, UT
    84112, USA
    Tel: 801 585 5606
    Fax: 801 585 7177
    Email: ddunn@genetics.utah.edu
    Insert Length: 10000 Std Error: 0.00
    Plate: 0009 row: M column: 20
    Seq primer: CGTTGTAAACACGCGCCAGT
    Class: plasmid ends
    High quality sequence stop: 34.
    Location/Qualifiers
    1..34
    /organism="Mus musculus"
    /strain="C57BL/6J"
    /db_xref="taxon:10090"
    /clone="UUGC2M0009M20"
    /clone_lib="Mouse 10kb plasmid UUGCLM library"
    /sex="Male"
    /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
    /note="Vector: PWD42nv; Purified genomic DNA from M.
    musculus C57BL/6J (male) was obtained from the Jackson
    Laboratory Mouse DNA Resource
    (http://www.jax.org/resources/documents/dnares/). The DNA
    was hydrodynamically sheared by repeated passage through a
    0.005 inch orifice at constant velocity. The sheared DNA
    was blunt end-repaired with T4 DNA polymerase and T4
    polynucleotide kinase. Adaptor oligonucleotides were
    ligated to the blunt ends in high molar excess. The
    adaptor DNA was purified and size-selected for a 9.5 to
    10.5 kb range using preparative agarose gel
    electrophoresis. Vector DNA was prepared from a derivative
    of pWD42 (G114732114|gb|AF129072.1), a copy-number
    inducible derivative of plasmid R1. The vector was ligated
    with adaptors complementary to the insert adaptors and
    purified. The sheared, adaptor mouse DNA was annealed to
    adaptor vector DNA, and transformed into
    chemically-competent E. coli XL10-Gold (Stratagene) cells
    and selected for ampicillin resistance."
    19 a 9 c 2 g 4 t
    BASE COUNT
    ORIGIN
    Query Match 85.5%; Score 9.4; DB 17; Length 34;
    Best Local Similarity 90.9%; Pred. No. 7.9e+04;
    Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTAACCCCTAAC 11
    ||||| |||||
Db 10 CTAACCTAAC 20

RESULT 11
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LOCUS
DEFINITION
    Arabidopsis thaliana 36 bp DNA linear GSS 18-JUN-2002
    genomic survey sequence.
ACCESSION
AL767851
VERSION
AL767851.1 GI:21520970
KEYWORDS
GSS.
SOURCE
    Arabidopsis thaliana
    thale cress.
    ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
    Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE
1
    Strizhov,N., Li,Y., Rosso,M., Viehoever,F., Dekker,K., Siedler,H.
    and Weisshaar,B.
    A pipeline for automated high-throughput generation of ESTs
    (flanking sequence tags) from Arabidopsis thaliana T-DNA

JOURNAL
COMMENT
    transformed lines
    Unpublished
    2
    Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B.
    A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
    for flanking sequence tag based reverse genetics
    Unpublished
    3
    (bases 1 to 36)
    Rosso,M., Strizhov,N., Li,Y. and Weisshaar,B.
    Direct Submission
    Submitted (17-JUN-2002) Weisshaar B., Max-Planck-Institut fuer
    Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
    This sequence is recovered from the left border of the T-DNA. It
    indicates an insertion within the locus defined by clone F28H19.
    The sequences are generated at the MPI for Plant Breeding Research
    in the context of the GABI-Kat project. GABI-Kat is part of the
    German Plant Genomics program designated 'GABI'. Information on
    line availability can be found at:
    http://www.mpiz-koeln.mpg.de/GABI-Kat/.
    Location/Qualifiers
    1..36
    /organism="Arabidopsis thaliana"
    /strain="Columbia 0"
    /db_xref="taxon:3702"
    /clone="GK-222E01-014236"
    /note="PCR was performed on DNA from Arabidopsis thaliana
    plants (T1) which were transformed with the T-DNA from
    vector pAG161. The lines contain one or more T-DNA
    insertions. The DNA fragment(s) resulting from the PCR
    were directly sequenced to determine the genomic sequence
    flanking the insertion. Sequences displaying significant
    similarity to the A. thaliana nuclear genome sequence were
    processed for submission. T-DNA derived sequences were
    removed"
    14 a 10 c 4 g 8 t
    BASE COUNT
    ORIGIN
    Query Match 85.5%; Score 9.4; DB 17; Length 36;
    Best Local Similarity 90.9%; Pred. No. 8e+04;
    Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTAACCCCTAAC 11
    ||||| |||||
Db 14 CTAACCCCTATC 24

RESULT 12
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LOCUS
DEFINITION
    Arabidopsis thaliana 39 bp mRNA linear EST 31-JUL-1998
    Schizosaccharomyces pombe cdna clone spc03845, mRNA sequence.
ACCESSION
AL767851
VERSION
AU008671.1 GI:3345129
KEYWORDS
EST.
SOURCE
    fission yeast.
    ORGANISM
    Schizosaccharomyces pombe
    Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
    Schizosaccharomycetales; Schizosaccharomycetaceae;
    Schizosaccharomycetes.
    1
    (bases 1 to 39)
    Morimyo,M. and Mita,K.
    Identification of expressed sequence tags of Schizosaccharomycetes
    pombe
    Unpublished (1998)
    Contact: Mitsuoki Morimyo
    Genome Research Group
    National Institute of Radiological Sciences
    9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
    Email: morimyo@nirs.go.jp.
    Location/Qualifiers
    1..39
    /organism="Schizosaccharomycetes pombe"
    source

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```

SOURCE
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1
Strizhov,N., Li,Y., Rosso,M., Viehoveer,P., Dekker,K., Saedler,H.
and Weisshaar,B.
A pipeline for automated high-throughput generation of ESTs
(flanking sequence tags) from Arabidopsis thaliana T-DNA
transformed lines
Unpublished
2
Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B.
A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
for flanking sequence tag based reverse genetics
Unpublished
3 (bases 1 to 31)
Strizhov,N., Rosso,M., Li,Y. and Weisshaar,B.
Direct Submission
Submitted (17-JUN-2002) Weisshaar B., Max-Planck-Institut fuer
Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence is recovered from the right border of the T-DNA. It
indicates an insertion close to or within gene Atg17190. The
sequences are generated at the MPI for Plant Breeding Research in
the context of the GABI-Kat project. GABI-Kat is part of the German
Plant Genomics program designated 'GABI'. Information on line
availability can be found at:
http://www.mpiz-koeln.mpg.de/GABI-Kat/.
FEATURES
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plants (T1) which were transformed with the T-DNA from
vector pAC161. The lines contain one or more T-DNA
insertions. The DNA fragment(s) resulting from the PCR
were directly sequenced to determine the genomic sequence
flanking the insertion. Sequences displaying significant
similarity to the A. thaliana nuclear genome sequence were
processed for submission. T-DNA derived sequences were
removed"
BASE COUNT 8 a 0 c 10 g 13 t
ORIGIN
Query Match 81.8%; Score 9; DB 17; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 AACCCCTAAC 11
Db 18 AACCCCTAAC 10
RESULT 15
LOCUS AU255689 32 bp mRNA linear EST 25-APR-2002
DEFINITION AU255689 3'-directed mouse cDNA library Mus musculus cDNA clone
BED0006171 3', mRNA sequence.
ACCESSION AU255689
VERSION AU255689.1 GI:20318670
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 32)
Kato,K. and Matoba,R.
Generation of expressed sequence tags from mouse brain
Unpublished (2002)

```

```

SOURCE
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1
Strizhov,N., Li,Y., Rosso,M., Viehoveer,P., Dekker,K., Saedler,H.
and Weisshaar,B.
A pipeline for automated high-throughput generation of ESTs
(flanking sequence tags) from Arabidopsis thaliana T-DNA
transformed lines
Unpublished
2
Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B.
A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
for flanking sequence tag based reverse genetics
Unpublished
3 (bases 1 to 31)
Strizhov,N., Rosso,M., Li,Y. and Weisshaar,B.
Direct Submission
Submitted (17-JUN-2002) Weisshaar B., Max-Planck-Institut fuer
Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence is recovered from the right border of the T-DNA. It
indicates an insertion close to or within gene Atg17190. The
sequences are generated at the MPI for Plant Breeding Research in
the context of the GABI-Kat project. GABI-Kat is part of the German
Plant Genomics program designated 'GABI'. Information on line
availability can be found at:
http://www.mpiz-koeln.mpg.de/GABI-Kat/.
FEATURES
source
1..31
Location/Qualifiers
/organism="Arabidopsis thaliana"
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/db_xref="taxon:3702"
/clone="GK-111H11-012331"
/notes="PCR was performed on DNA from Arabidopsis thaliana
plants (T1) which were transformed with the T-DNA from
vector pAC161. The lines contain one or more T-DNA
insertions. The DNA fragment(s) resulting from the PCR
were directly sequenced to determine the genomic sequence
flanking the insertion. Sequences displaying significant
similarity to the A. thaliana nuclear genome sequence were
processed for submission. T-DNA derived sequences were
removed"
BASE COUNT 8 a 0 c 10 g 13 t
ORIGIN
Query Match 81.8%; Score 9; DB 17; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 AACCCCTAAC 11
Db 18 AACCCCTAAC 10
RESULT 15
LOCUS AU255689 32 bp mRNA linear EST 25-APR-2002
DEFINITION AU255689 3'-directed mouse cDNA library Mus musculus cDNA clone
BED0006171 3', mRNA sequence.
ACCESSION AU255689
VERSION AU255689.1 GI:20318670
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 32)
Kato,K. and Matoba,R.
Generation of expressed sequence tags from mouse brain
Unpublished (2002)

```

COMMENT

Contact: Kikuya Kato
Graduate School of Biological Sciences
Nara Institute of Science and Technology
8916-5 Takayama Ikoma, Nara 630-0101, Japan
Tel: 81-743-72-5581
Fax: 81-743-72-5589
Email: kkatobs.aist-nara.ac.jp,
URL: <http://love2.aist-nara.ac.jp/BED/index.html>.

FEATURES

Source
1..32
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/clone="BED0006171"
/clone_lib="3'-directed mouse cDNA library"
/tissue_type="brain"
/note="Vector: pGEM-T-easy"

BASE COUNT
ORIGIN

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Query Match 81.8%; Score 9; DB 9; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TAACCCCTAA 10
|||||
Db 23 TAACCCCTAA 31

Search completed: July 6, 2003, 09:39:47
Job time : 1645.18 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 6, 2003, 06:42:31 ; Search time 522.5 Seconds
(without alignments)
612.691 Million cell updates/sec

Title: US-09-540-843-9
Perfect score: 11
Sequence: 1 ctaaccctaac 11

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 774614

Minimum DB seq length: 0
Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*
2: gb_htg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*
15: em_ba.*
16: em_fun.*
17: em_hum.*
18: em_in.*
19: em_mu.*
20: em_om.*
21: em_or.*
22: em_ov.*
23: em_pat.*
24: em_ph.*
25: em_pl.*
26: em_ro.*
27: em_sts.*
28: em_un.*
29: em_vi.*
30: em_htg_hum.*
31: em_htg_inv.*
32: em_htg_other.*
33: em_htg_mus.*
34: em_htg_pin.*
35: em_htg_rod.*
36: em_htg_mam.*
37: em_htg_vrt.*
38: em_sy.*
39: em_hugo_hum.*
40: em_hugo_mus.*
41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	11	100.0	11	6	AR016034	Sequence
2	11	100.0	11	6	AR026486	Sequence
3	11	100.0	11	6	AR026487	Sequence
4	11	100.0	11	6	AR059195	Sequence
5	11	100.0	11	6	AR075506	Sequence
6	11	100.0	11	6	AR161904	Sequence
7	11	100.0	11	6	AX033373	Sequence
8	11	100.0	11	6	AX268757	Sequence
9	11	100.0	11	6	AX268761	Sequence
10	11	100.0	11	6	AX283296	Sequence
11	11	100.0	11	6	I31749	Sequence 2
12	11	100.0	15	6	AR026479	Sequence
13	11	100.0	16	6	AR050942	Sequence
14	11	100.0	16	6	AR204610	Sequence
15	11	100.0	16	6	I51743	Sequence 11
16	11	100.0	17	6	A84605	Sequence 15
17	11	100.0	17	6	AR026488	Sequence
18	11	100.0	17	6	AR145675	Sequence
19	11	100.0	17	6	AR145676	Sequence
20	11	100.0	18	6	A79654	Sequence 3
21	11	100.0	18	6	A79665	Sequence 14
22	11	100.0	18	6	A84598	Sequence 8
23	11	100.0	18	6	A84599	Sequence 9
24	11	100.0	18	6	AR016059	Sequence
25	11	100.0	18	6	AR026482	Sequence
26	11	100.0	18	6	AR026483	Sequence
27	11	100.0	18	6	AR026484	Sequence
28	11	100.0	18	6	AR037860	Sequence
29	11	100.0	18	6	AR037861	Sequence
30	11	100.0	18	6	AR037862	Sequence
31	11	100.0	18	6	AR050936	Sequence
32	11	100.0	18	6	AR050962	Sequence
33	11	100.0	18	6	AR053263	Sequence
34	11	100.0	18	6	AR054739	Sequence
35	11	100.0	18	6	AR054740	Sequence
36	11	100.0	18	6	AR054741	Sequence
37	11	100.0	18	6	AR059509	Sequence
38	11	100.0	18	6	AR059546	Sequence
39	11	100.0	18	6	AR059547	Sequence
40	11	100.0	18	6	AR069393	Sequence
41	11	100.0	18	6	AR069394	Sequence
42	11	100.0	18	6	AR069395	Sequence
43	11	100.0	18	6	AR075504	Sequence
44	11	100.0	18	6	AR079895	Sequence
45	11	100.0	18	6	AR079896	Sequence

ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION Sequence 2 from patent US 5776679.
ACCESSION AR016034
VERSION AR016034.1 GI:3972311
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 11)
AUTHORS Villeponteau, B., Feng, J., Funk, W. and Andrews, W.H.
TITLE Assays for the DNA component of human telomerase
JOURNAL Patent: US 5776679-A 2 07-JUL-1998;
FEATURES Location/Qualifiers

AR016034 11 bp DNA linear PAT 05-DEC-1998
Sequence 2 from patent US 5776679.
AR016034
AR016034.1 GI:3972311
Unknown.
Unclassified.
1 (bases 1 to 11)
Villeponteau, B., Feng, J., Funk, W. and Andrews, W.H.
Assays for the DNA component of human telomerase
Patent: US 5776679-A 2 07-JUL-1998;
Location/Qualifiers

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BASE COUNT 4 a 5 c 0 g 2 t
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Best Local Similarity 100.0%; Pred. No. 2.5e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 CTAACCCCTAAC 11

RESULT 2
AR026486/c
LOCUS AR026486 11 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 11 from patent US 5856096.
ACCESSION AR026486
VERSION AR026486.1 GI:5937326
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 11)
AUTHORS Windle,B.E., Qiu,M., Chen,S.-F., Fletcher,T.M. and Maine,I.
TITLE Rapid and sensitive assays for detecting and distinguishing between
processive and non-processive telomerase activities
JOURNAL Patent: US 5856096-A 11 05-JAN-1999;
FEATURES Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 2.5e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
AR026487
LOCUS AR026487 11 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 12 from patent US 5856096.
ACCESSION AR026487
VERSION AR026487.1 GI:5937327
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 11)
AUTHORS Windle,B.E., Qiu,M., Chen,S.-F., Fletcher,T.M. and Maine,I.
TITLE Rapid and sensitive assays for detecting and distinguishing between
processive and non-processive telomerase activities
JOURNAL Patent: US 5856096-A 12 05-JAN-1999;
FEATURES Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 2.5e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 CTAACCCCTAAC 11

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Best Local Similarity 100.0%; Pred. No. 2.5e+04;
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Db 1 CTAACCCCTAAC 11

RESULT 4
AR059195
LOCUS AR059195 11 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 2 from patent US 5837857.
ACCESSION AR059195
VERSION AR059195.1 GI:5984772
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 11)
AUTHORS Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
TITLE Mammalian telomerase
JOURNAL Patent: US 5837857-A 2 17-NOV-1998;
FEATURES Location/Qualifiers
source 1. .11
BASE COUNT 4 a 5 c 0 g 2 t
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 2.5e+04;
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Qy 1 CTAACCCCTAAC 11
Db 1 CTAACCCCTAAC 11

RESULT 5
AR075506
LOCUS AR075506 11 bp DNA linear PAT 30-AUG-2000
DEFINITION Sequence 3 from patent US 5958680.
ACCESSION AR075506
VERSION AR075506.1 GI:10002256
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 11)
AUTHORS Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
TITLE Mammalian telomerase
JOURNAL Patent: US 5958680-A 3 28-SEP-1999;
FEATURES Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 2.5e+04;
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Db 1 CTAACCCCTAAC 11

RESULT 6
AR161904
LOCUS AR161904 11 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 2 from patent US 6258535.
ACCESSION AR161904
VERSION AR161904.1 GI:16228913
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 11)
AUTHORS Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
TITLE Mammalian telomerase
JOURNAL Patent: US 6258535-A 2 10-JUL-2001;
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Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CTAACCCCTAAC 11
Db      |||||
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RESULT 7
AX033373
LOCUS      AX268761      11 bp      mRNA      linear      PAT 21-SEP-2000
DEFINITION Sequence 5 from Patent WO0046601.
ACCESSION  AX033373
VERSION     AX033373.1 GI:10280147
KEYWORDS   human.
SOURCE     Homo sapiens
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS    Larsen,F. and Skaenseng,M.
TITLE      Detecting telomerase activity
JOURNAL    Patent: WO 0046601-A 5 10-AUG-2000;
LARSSEN FRANK (NO) ; SKAENSENG MARIANNE (NO)
FEATURES   Location/Qualifiers
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    1. .11
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RESULT 8
AX268757/c
LOCUS      AX268757      11 bp      DNA      linear      PAT 29-OCT-2001
DEFINITION Sequence 5 from Patent WO0174342.
ACCESSION  AX268757
VERSION     AX268757.1 GI:16541829
KEYWORDS   synthetic construct.
SOURCE     synthetic construct.
ORGANISM   artificial sequences.
REFERENCE  1
AUTHORS    Gilchrest,B.A., Yaar,M. and Eller,M.
TITLE      Use of locally applied dna fragments
JOURNAL    Patent: WO 0174342-A 5 11-OCT-2001;
TRUSTEES OF BOSTON UNIVERSITY (US)
FEATURES   Location/Qualifiers
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    1. .11
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    /note="Synthetic DNA Fragment"
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ORIGIN

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Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      |||||
11 CTAACCCCTAAC 11

RESULT 9
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LOCUS      AX268761      11 bp      DNA      linear      PAT 29-OCT-2001
DEFINITION Sequence 9 from Patent WO0174342.
ACCESSION  AX268761
VERSION     AX268761.1 GI:16541833
KEYWORDS   synthetic construct.
SOURCE     synthetic construct.
ORGANISM   artificial sequences.
REFERENCE  1
AUTHORS    Gilchrest,B.A., Yaar,M. and Eller,M.
TITLE      Use of locally applied dna fragments
JOURNAL    Patent: WO 0174342-A 9 11-OCT-2001;
TRUSTEES OF BOSTON UNIVERSITY (US)
FEATURES   Location/Qualifiers
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Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 10
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LOCUS      AX283296      11 bp      DNA      linear      PAT 20-NOV-2001
DEFINITION Sequence 60 from Patent WO0179249.
ACCESSION  AX283296
VERSION     AX283296.1 GI:17044177
KEYWORDS   synthetic construct.
SOURCE     synthetic construct.
ORGANISM   artificial sequences.
REFERENCE  1
AUTHORS    Uhlmann,E., Breipohl,G. and Will,D.W.
TITLE      Polyamide nucleic acid derivatives, agents and methods for
JOURNAL    producing the same
JOURNAL    Patent: WO 0179249-A 60 25-OCT-2001;
Aventis Pharma Deutschland GmbH (DE)
FEATURES   Location/Qualifiers
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Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      |||||
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RESULT 11

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I31749
LOCUS I31749 11 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 2 from patent US 5583016.
ACCESSION I31749
VERSION I31749.1 GI:1822540
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 11)
AUTHORS Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
TITLE Mammalian telomerase
JOURNAL Patent: US 5583016-A 2 10-DEC-1996;
FEATURES Location/Qualifiers
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Query Match 100.0%; Score 11; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+04; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 CTAACCCCTAAC 11
RESULT 12
AR026479
LOCUS AR026479 15 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 4 from patent US 5856096.
ACCESSION AR026479
VERSION AR026479.1 GI:5937319
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Windle,B.E., Olu,M., Chen,S.-F., Fletcher,T.M. and Maine,I.
TITLE Rapid and sensitive assays for detecting and distinguishing between
processive and non-processive telomerase activities
JOURNAL Patent: US 5856096-A 4 05-JAN-1999;
FEATURES Location/Qualifiers
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Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 3 CTAACCCCTAAC 13
RESULT 13
AR050942
LOCUS AR050942 16 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 11 from patent US 5830644.
ACCESSION AR050942
VERSION AR050942.1 GI:5974306
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS West,M.D., Shay,J. and Wright,W.E.
TITLE Method for screening for agents which increase telomerase activity
JOURNAL Patent: US 5830644-A 11 03-NOV-1998;

FEATURES Location/Qualifiers
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Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 3 CTAACCCCTAAC 13
RESULT 14
AR204610
LOCUS AR204610 16 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 60 from patent US 6368789.
ACCESSION AR204610
VERSION AR204610.1 GI:21501980
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS West,M.D., Shay,J., Wright,W. and Blackburn,E.H.
TITLE Screening methods to identify inhibitors of telomerase activity
JOURNAL Patent: US 6368789-A 60 09-APR-2002;
FEATURES Location/Qualifiers
source 1..16
BASE COUNT 4 a 9 c 0 g 3 t
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 2.3e+04; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTAACCCCTAAC 11
Db 3 CTAACCCCTAAC 13
RESULT 15
I51743
LOCUS I51743 16 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 11 from patent US 5645986.
ACCESSION I51743
VERSION I51743.1 GI:2472944
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS West,M.D., Harley,C.B., Strahl,C.M., McEachern,M.J., Shay,J.,
Wright,W.E., Blackburn,E.H. and Vaziri,H.
TITLE Therapy and diagnosis of conditions related to telomere length
and/or telomerase activity
JOURNAL Patent: US 5645986-A 11 08-JUL-1997;
FEATURES Location/Qualifiers
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BASE COUNT 4 a 9 c 0 g 3 t
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Db 3 CTAACCCCTAAC 13

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Job time : 524.5 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 6, 2003, 06:40:37 ; Search time 243.571 Seconds
(without alignments)
101.703 Million cell updates/sec

Title: US-09-540-843-9

Perfect score: 11

Sequence: 1 ctaaccctaac 11

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SUMMARIES

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c 2	11	100.0	11	18	AAH89250
c 3	11	100.0	11	18	AAH89237
c 4	11	100.0	11	18	AAH90060
c 5	11	100.0	11	21	AAA37556
c 6	11	100.0	11	21	AAA37561
c 7	11	100.0	11	21	AAA37562
c 8	11	100.0	11	21	AAA37573
c 9	11	100.0	11	21	AAA37586

c 10	11	100.0	11	22	AAF81185	Oligonucleotide th
c 11	11	100.0	11	22	AAH26728	Phosphoramidate-li
c 12	11	100.0	11	22	AAH26732	Phosphoramidate-li
c 13	11	100.0	11	23	AAH14909	Melanogenesis asso
c 14	11	100.0	11	23	AAH14913	Melanogenesis asso
c 15	11	100.0	11	23	AAH15434	PNA 7/1V inhibiti
c 16	11	100.0	11	23	AAH15450	Oligonucleotide #6
c 17	11	100.0	11	23	AAH15457	Phosphorothioate (
c 18	11	100.0	11	24	AAH98619	Modified peptide n
c 19	11	100.0	11	24	AAH97513	Peptide nucleic ac
c 20	11	100.0	12	18	AAH89232	Peptide nucleic ac
c 21	11	100.0	12	21	AAH37551	PNA sequence #8 us
c 22	11	100.0	12	23	AAH15429	PNA V inhibiting h
c 23	11	100.0	12	23	ABH05288	Oligonucleotide pr
c 24	11	100.0	12	23	ABH34202	Oligonucleotide pr
c 25	11	100.0	13	18	AAH89225	Peptide nucleic ac
c 26	11	100.0	13	18	AAH89236	Peptide nucleic ac
c 27	11	100.0	13	21	AAH37544	Peptide nucleic ac
c 28	11	100.0	13	21	AAH37555	PNA sequence #12 u
c 29	11	100.0	13	22	AAH81195	Thiophosphoramidat
c 30	11	100.0	13	23	AAH15423	PNA 8/VI inhibiti
c 31	11	100.0	13	23	AAH15433	PNA 6/X inhibiti
c 32	11	100.0	13	23	ABH19880	Oligonucleotide SE
c 33	11	100.0	13	23	ABH19881	Oligonucleotide SE
c 34	11	100.0	13	23	ABH02802	Oligonucleotide SE
c 35	11	100.0	13	23	ABH02803	Oligonucleotide SE
c 36	11	100.0	15	18	AAH89226	Peptide nucleic ac
c 37	11	100.0	15	18	AAH89229	Peptide nucleic ac
c 38	11	100.0	15	18	AAH90068	Telomerase primer
c 39	11	100.0	15	21	AAH37545	PNA sequence #2 us
c 40	11	100.0	15	21	AAH37548	PNA sequence #5 us
c 41	11	100.0	15	21	AAH37587	Antisense sequence
c 42	11	100.0	15	23	AAH15424	PNA VII inhibiti
c 43	11	100.0	15	23	AAH15427	PNA XIII inhibiti
c 44	11	100.0	15	23	AAH15458	Phosphorothioate (
c 45	11	100.0	16	16	AAH01177	Telomeric repeat-b

ALIGNMENTS

RESULT 1
AAV07769/c
ID AAV07769 standard; DNA; 11 BP.
XX
AC AAV07769;
XX
DT 07-DEC-1998 (first entry)
XX
DE N3 to P5 oligonucleotide phosphoramidate useful as telomerase inhibitor.
DE telomerase inhibitor; phosphoramidate; telomerase-binding region; TBR;
KW cell proliferation; tumour; lukaemia; duplex; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 1..11
FT /tag= a
FT /note= "each linkage is a phosphoramidate linkage"

XX
PN W09737691-A1.
XX
PD 16-OCT-1997.
XX
PF 08-APR-1997; 97WO-US05773.
XX
PR 10-APR-1996; 96US-0630242.
XX
PA (LYNX-) LYNX THERAPEUTICS INC.
XX
PI Lloyd DH;
XX

DR WPI; 1997-512422/47.
XX
PT Treating elevated telomerase levels with N3 to P5 oligonucleotide
PT phosphoramidates - that bind to the RNA component of telomerase,
PT specifically for preventing growth of cancer cells, fungi and
PT protozoa
XX
PS Claim 5; Page 25; 38pp; English.
XX
CC The invention relates to treatment of conditions associated with high
CC levels of telomerase activity in a cell. The treatment comprises
CC administering an oligonucleotide N3' -> P5' phosphoramidate having a
CC sequence complementary to part of the telomere-binding region (TBR) of
CC the RNA component of telomerase, so as to inhibit its activity. The
CC N3' -> P5' oligonucleotide phosphoramidates are used therapeutically to
CC inhibit cell proliferation, e.g. against a wide range of solid tumours
CC or leukaemia, and also against fungal and protozoal pathogens. They are
CC soluble and resistant to nuclease, and they bind strongly to RNA forming
CC short but stable duplexes under physiological conditions. Thus they are
CC very effective and selective inhibitors of telomerase. The present
CC sequence represents a specific example of an oligonucleotide N3' -> P5'
CC phosphoramidate disclosed in the specification.
XX
SQ Sequence 11 BP; 2 A; 0 C; 5 G; 4 T; 0 other;
Query Match 100.0%; Score 11; DB 18; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTAACCCCTAAC 11
Db 11 CTAACCCCTAAC 1
RESULT 2
ID AAT89250 standard; DNA; 11 BP.
XX
AC AAT89250;
XX
DT 12-MAY-1998 (first entry)
XX
DE DNA oligonucleotide 6, used in the measurement of Tm values.
XX
KW Peptide nucleic acid; PNA; cancer; telomerase; probe; hybridisation;
KW inhibitor; human telomerase RNA; htr; PCR; oligonucleotide; ss.
XX
OS Synthetic.
XX
PN WO9738013-A1.
XX
PD 16-OCT-1997.
XX
PF 09-APR-1997; 97WO-US05931.
XX
PR 09-APR-1996; 96US-0630019.
XX
PA (GERO-) GERON CORP.
XX
PI Corey D, Norton JC, Piatyszek MA, Shay JW, Wright WE;
XX
DR WPI; 1997-512647/47.
XX
PT New peptide nucleic acids hybridising to mammalian telomerase RNA -
PT used to inhibit telomerase, for treating tumours and other
PT proliferative diseases, also for diagnosis
XX
PS Example 2; Page 49; 76pp; English.
XX
CC This is an oligonucleotide used in the measurement of Tm values and
CC their complementary peptide nucleic acids (PNAs), (e.g.
CC AAT89231-T89240). PNAs hybridise specifically to an RNA component of
CC mammalian telomerase, and include the sequence GGG for specific

CC hybridisation to the template region of this component. PNAs can be used
CC as probes to detect the RNA component of mammalian telomerase and as
CC inhibitors of telomerase activity, especially in the treatment of
CC cancer.
XX
SQ Sequence 11 BP; 4 A; 5 C; 0 G; 2 T; 0 other;
Query Match 100.0%; Score 11; DB 18; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTAACCCCTAAC 11
Db 1 CTAACCCCTAAC 11
RESULT 3
ID AAT89237/C
XX
AC AAT89237;
XX
DT 12-MAY-1998 (first entry)
XX
DE Peptide nucleic acid 12, targeted to mammalian telomerase.
XX
KW Peptide nucleic acid; PNA; cancer; telomerase; probe; hybridisation;
KW inhibitor; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..13 /tag= a
FT /note= "Sugar-phosphate backbone has been replaced by
FT modified_base 1 /tag= b
FT /note= "Optionally conjugated to peptide AAW31919"
FT modified_base 13 /tag= c
FT /note= "Optionally conjugated to peptide AAW31919"
XX
PN WO9738013-A1.
XX
PD 16-OCT-1997.
XX
PF 09-APR-1997; 97WO-US05931.
XX
PR 09-APR-1996; 96US-0630019.
XX
PA (GERO-) GERON CORP.
XX
PI Corey D, Norton JC, Piatyszek MA, Shay JW, Wright WE;
XX
DR WPI; 1997-512647/47.
XX
PT New peptide nucleic acids hybridising to mammalian telomerase RNA -
PT used to inhibit telomerase, for treating tumours and other
PT proliferative diseases, also for diagnosis
XX
PS Claim 9; Page 59; 76pp; English.
XX
CC This sequence is a novel peptide nucleic acid (PNA), which acts as
CC an inhibitor of mammalian, preferably human, telomerase. The PNAs
CC hybridise specifically to an RNA component of mammalian telomerase,
CC and include the sequence GGG for specific hybridisation to the template
CC region of this component. PNAs can be used as probes to detect the
CC RNA component of mammalian telomerase and as inhibitors of telomerase
CC activity, especially in the treatment of cancer.
XX
SQ Sequence 11 BP; 2 A; 0 C; 5 G; 4 T; 0 other;

Query Match 100.0%; Score 11; DB 18; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTAACCCCTAAC 11
 |||||
 Db 11 CTAACCCCTAAC 1

RESULT 4
 AAT90060/C
 ID AAT90060 standard; DNA; 11 BP.
 XX
 AC AAT90060;
 XX
 DT 24-NOV-1997 (first entry)
 XX
 DE Telomerase primer.
 XX
 KW Detection; telomerase; amplification; polymerase chain reaction;
 KW PCR; primer; cancer; carcinoma; sarcoma; leukaemia; leukemia;
 KW myeloma; lymphoma; neuroblastoma; astrocytoma; glioma;
 KW glioblastoma; retinoblastoma; melanoma; screen; drug;
 KW determination; telomere length; ss.
 XX
 OS Synthetic.
 XX
 PN WO9711198-A1.
 XX
 PD 27-MAR-1997.
 XX
 PF 20-SEP-1996; 96WO-US15162.
 XX
 PR 20-SEP-1995; 95US-0531743.
 XX
 PA (CTRC-) CTRC RES FOUND.
 XX
 PI Chen S, Fletcher TM, Maine I, Qiu M, Windle BE;
 XX WPI; 1997-202904/18.
 DR
 XX Detecting telomerase activity by ligation sequential reaction -
 PT useful for diagnosis of cancer or to screen for telomerase
 PT inhibitors
 XX
 PS Claim 40; Page 27; 71pp; English.
 XX
 CC A novel method of detecting telomerase activity in a sample, the
 CC comprises amplifying a sample with a telomerase primer, e.g. the
 CC present sequence, and contacting the product with 1st and 2nd
 CC oligonucleotides, which hybridise to the product so that no single
 CC stranded region intervenes between them. The hybridised product and
 CC oligonucleotides are then contacted with ligase and the ligated
 CC form of the oligonucleotides detected.
 CC The method can be used to detect cancer, e.g. carcinomas of the
 CC breast, colon, oesophagus, kidney, liver, lung, ovaries, prostate,
 CC stomach, uterus, pancreas and head and neck, sarcomas of bone and
 CC muscle, leukaemias, myelomas, lymphomas, neuroblastomas,
 CC astrocytomas, gliomas, glioblastomas, retinoblastomas and
 CC melanomas. The method can also be used to screen for
 CC anti-telomerase activity in candidate drugs and to determine
 CC telomere length.
 XX
 SQ Sequence 11 BP; 2 A; 0 C; 5 G; 4 T; 0 other;

Query Match 100.0%; Score 11; DB 18; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTAACCCCTAAC 11
 |||||
 Db 11 CTAACCCCTAAC 1

RESULT 5
 AAA37556/C
 ID AAA37556 standard; DNA; 11 BP.
 XX
 AC AAA37556;
 XX
 DT 15-AUG-2000 (first entry)
 XX
 DE PNA sequence #13 used to inhibit telomerase activity.
 XX
 KW Peptide nucleic acid; PNA; telomerase; ribonucleoprotein enzyme; cancer;
 KW inhibitor; neoplasia; neurodegenerative disease; aging; hyperplasia;
 KW AIDS; HIV; fungal infection; forensic identification; detect; tumour;
 KW paternity testing; ss.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT misc_feature 1..11
 FT /*tag= a
 FT /note= "Peptide nucleic acid molecule, where
 FT N-(2-aminoethyl)glycine units are linked to
 FT nucleotide bases via glycine amino N through a
 FT methylenecarbonyl linker"
 XX
 PN US6046307-A.
 XX
 PD 04-APR-2000.
 XX
 PF 09-APR-1997; 97US-0838545.
 XX
 PR 09-APR-1996; 96US-0630019.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Wright WE, Platyszek MA, Shay JW, Norton JC, Corey DR;
 XX WPI; 2000-292432/25.
 DR
 XX New peptide nucleic acid (PNA) compounds that inhibit telomerase
 PT activity in mammalian cells is useful as probes to detect the RNA
 PT component of a mammalian telomerase
 XX
 PS Claim 6; Column 71; 45pp; English.
 XX
 CC The present sequence represents a peptide nucleic acid molecule which
 CC hybridises to the mRNA component of mammalian telomerase, and inhibits
 CC telomerase activity. Telomerase is a ribonucleoprotein enzyme that
 CC synthesizes one strand of the telomeric DNA, using as a template an 11
 CC nucleotide sequence contained within the RNA component of the enzyme. The
 CC invention relates to PNA molecules having a sequence of no more than 25
 CC bases, which include the sequence GTTAGG. The uncharged nature of the PNA
 CC backbone increases the melting temperature of associating strands,
 CC increases the rate of association with targeted nucleic acids, and
 CC affords greater resistance of degradation by proteases or nucleases. The
 CC therapeutic PNAs may be used for treating disease conditions such as
 CC cancers, neoplasia, hyperplasia, neurodegenerative diseases, aging, human
 CC immunodeficiency virus (HIV) infection/AIDS (acquired immunodeficiency
 CC syndrome) and associated pathologies, fungal infections, and other
 CC diseases characterized by abnormal telomere metabolism or telomerase
 CC activity, in combination with antineoplastic and other cytotoxic or
 CC cytostatic agents, antifungal agents, and other nucleotides. PNAs may be
 CC used for molecular diagnostics, labelled PNAs are used as hybridization
 CC probes to detect or quantitate polynucleotides having a human telomerase
 CC RNA (hTR) sequence. PNA probes are also used for forensic identification
 CC of individuals, e.g. paternity testing, based on hTR gene restriction
 CC fragment length polymorphism (RFLP) pattern. PNAs are also useful as
 CC probes to detect the RNA component of a mammalian telomerase and as
 CC inhibitors of telomerase activity. The method of the present invention
 CC allows cancerous conditions to be detected with increased confidence and
 CC possibly at an earlier stage, before cells are detected as cancerous
 CC based on pathological characteristics. The diagnostic and prognostic

CC methods of the present invention can be used to detect an immortal or
 CC neoplastic cell or tumour tissue or cancer of any origin, provided the
 CC cell expresses telomerase activity and its RNA component.
 XX
 SQ Sequence 11 BP; 2 A; 0 C; 5 G; 4 T; 0 other;
 Query Match 100.0%; Score 11; DB 21; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CTAACCCCTAAC 11
 Db 11 CTAACCCCTAAC 1
 RESULT 6
 AAA37561/c
 ID AAA37561 standard; DNA; 11 BP.
 AC AAA37561;
 XX
 DT 15-AUG-2000 (first entry)
 DE PNA sequence #18 used to inhibit telomerase activity.
 KW Peptide nucleic acid; PNA; telomerase; ribonucleoprotein enzyme; cancer;
 KW inhibitor; neoplasia; neurodegenerative disease; aging; hyperplasia;
 KW AIDS; HIV; fungal infection; forensic identification; detect; tumour;
 KW paternity testing; ss.
 XX
 OS Synthetic.
 FH Key Location/Qualifiers
 FT misc_feature 1..11
 FT /tag= a
 FT /note= "Peptide nucleic acid molecule, where
 FT N-(2-aminoethyl)glycine units are linked to
 FT nucleotide bases via glycine amino N through a
 FT methylenecarbonyl linker"
 FT
 FT misc_feature 1
 FT /tag= b
 FT /note= "G residue is linked to the carboxy end of the
 FT peptide GGRQIKIWFQNMKWKK"
 FT
 FT
 FT
 PN US6046307-A.
 XX
 XX 04-APR-2000.
 XX
 XX 09-APR-1997; 97US-0838545.
 XX
 XX (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Wright WE, Piatyszek MA, Shay JW, Norton JC, Corey DR;
 XX WPI; 2000-292432/25.
 XX
 XX New peptide nucleic acid (PNA) compounds that inhibit telomerase
 PT activity in mammalian cells is useful as probes to detect the RNA
 PT component of a mammalian telomerase
 XX
 XX Claim 9; Column 71-72; 45pp; English.
 XX
 CC The present sequence represents a peptide nucleic acid molecule which
 CC hybridises to the mRNA component of mammalian telomerase, and inhibits
 CC telomerase activity. Telomerase is a ribonucleoprotein enzyme that
 CC synthesizes one strand of the telomeric DNA, using as a template an 11
 CC nucleotide sequence contained within the RNA component of the enzyme. The
 CC invention relates to PNA molecules having a sequence of no more than 25
 CC bases, which include the sequence GTTAGG. The uncharged nature of the PNA
 CC backbone increases the melting temperature of associating strands, and
 CC increases the rate of association with targeted nucleic acids, and

CC affords greater resistance of degradation by proteases or nucleases. The
 CC therapeutic PNAs may be used for treating disease conditions such as
 CC cancers, neoplasia, hyperplasia, neurodegenerative diseases, aging, human
 CC immunodeficiency virus (HIV) infection/AIDS (acquired immunodeficiency
 CC syndrome) and associated pathologies, fungal infections, and other
 CC diseases characterized by abnormal telomere metabolism or telomerase
 CC activity, in combination with antineoplastic and other cytotoxic or
 CC cytostatic agents, antifungal agents, and other nucleotides. PNAs may be
 CC used for molecular diagnostics, labelled PNAs are used as hybridization
 CC probes to detect or quantitate polynucleotides having a human telomerase
 CC RNA (hTR) sequence. PNA probes are also used for forensic identification
 CC of individuals, e.g. paternity testing, based on hTR gene restriction
 CC fragment length polymorphism (RFLP) pattern. PNAs are also useful as
 CC probes to detect the RNA component of a mammalian telomerase and as
 CC inhibitors of telomerase activity. The method of the present invention
 CC allows cancerous conditions to be detected with increased confidence and
 CC possibly at an earlier stage, before cells are detected as cancerous
 CC based on pathological characteristics. The diagnostic and prognostic
 CC methods of the present invention can be used to detect an immortal or
 CC neoplastic cell or tumour tissue or cancer of any origin, provided the
 CC cell expresses telomerase activity and its RNA component.
 XX
 SQ Sequence 11 BP; 2 A; 0 C; 5 G; 4 T; 0 other;
 Query Match 100.0%; Score 11; DB 21; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CTAACCCCTAAC 11
 Db 11 CTAACCCCTAAC 1
 RESULT 7
 AAA37562/c
 ID AAA37562 standard; DNA; 11 BP.
 XX
 AC AAA37562;
 XX
 DT 15-AUG-2000 (first entry)
 DE PNA sequence #19 used to inhibit telomerase activity.
 XX
 KW Peptide nucleic acid; PNA; telomerase; ribonucleoprotein enzyme; cancer;
 KW inhibitor; neoplasia; neurodegenerative disease; aging; hyperplasia;
 KW AIDS; HIV; fungal infection; forensic identification; detect; tumour;
 KW paternity testing; ss.
 XX
 OS Synthetic.
 FH Key Location/Qualifiers
 FT misc_feature 1..11
 FT /tag= a
 FT /note= "Peptide nucleic acid molecule, where
 FT N-(2-aminoethyl)glycine units are linked to
 FT nucleotide bases via glycine amino N through a
 FT methylenecarbonyl linker"
 FT
 FT misc_feature 11
 FT /tag= b
 FT /note= "G residue is linked to the amino end of the
 FT peptide GGRQIKIWFQNMKWKK"
 FT
 FT
 PN US6046307-A.
 XX
 XX 04-APR-2000.
 XX
 XX '09-APR-1997; 97US-0838545.
 XX
 XX '09-APR-1996; 96US-0630019.
 XX
 XX (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Wright WE, Piatyszek MA, Shay JW, Norton JC, Corey DR;

XX WPI; 2000-292432/25.

XX New peptide nucleic acid (PNA) compounds that inhibit telomerase

PT activity in mammalian cells is useful as probes to detect the RNA

PT component of a mammalian telomerase

XX

XX Claim 9; Column 71-72; 45pp; English.

XX

CC The present sequence represents a peptide nucleic acid molecule which

CC hybridises to the mRNA component of mammalian telomerase, and inhibits

CC telomerase activity. Telomerase is a ribonucleoprotein enzyme that

CC synthesizes one strand of the telomeric DNA, using as a template an 11

CC nucleotide sequence contained within the RNA component of the enzyme. The

CC invention relates to PNA molecules having a sequence of no more than 25

CC bases, which include the sequence GTTAGG. The uncharged nature of the PNA

CC backbone increases the melting temperature of associating strands,

CC increases the rate of association with targeted nucleic acids, and

CC affords greater resistance of degradation by proteases or nucleases. The

CC therapeutic PNAs may be used for treating disease conditions such as

CC cancers, neoplasia, hyperplasia, neurodegenerative diseases, aging, human

CC immunodeficiency virus (HIV) infection/AIDS (acquired immunodeficiency

CC syndrome) and associated pathologies, fungal infections, and other

CC diseases characterized by abnormal telomere metabolism or telomerase

CC activity, in combination with antineoplastic and other cytotoxic or

CC cytostatic agents, antifungal agents, and other nucleotides. PNAs may be

CC used for molecular diagnostics, labelled PNAs are used as hybridization

CC probes to detect or quantitate polynucleotides having a human telomerase

CC RNA (hTR) sequence. PNA probes are also used for forensic identification

CC of individuals, e.g. paternity testing, based on hTR gene restriction

CC fragment length polymorphism (RFLP) pattern. PNAs are also useful as

CC probes to detect the RNA component of a mammalian telomerase and as

CC inhibitors of telomerase activity. The method of the present invention

CC allows cancerous conditions to be detected with increased confidence and

CC possibly at an earlier stage, before cells are detected as cancerous

CC based on pathological characteristics. The diagnostic and prognostic

CC methods of the present invention can be used to detect an immortal or

CC neoplastic cell or tumour tissue or cancer of any origin, provided the

CC cell expresses telomerase activity and its RNA component.

XX

XX Sequence 11 BP; 2 A; 0 C; 5 G; 4 T; 0 other;

XX

Query Match 100.0%; Score 11; DB 21; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.7e+03;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTAACCCCTAAC 11

DB 11 CTAACCCCTAAC 1

RESULT 8

AAA37573

ID AAA37573 standard; DNA; 11 BP.

XX

XX AAA37573;

XX

XX 15-AUG-2000 (first entry)

XX

DE PNA sequence #31 used to inhibit telomerase activity.

XX

KW Peptide nucleic acid; PNA; telomerase; ribonucleoprotein enzyme; cancer;

KW inhibitor; neoplasia; neurodegenerative disease; aging; hyperplasia;

KW AIDS; HIV; fungal infection; forensic identification; detect; tumour;

KW paternity testing; ss.

XX

OS Synthetic.

XX

XX Key Location/Qualifiers

FT misc_feature 1..11

FT /*tag=

FT /note= "Peptide nucleic acid molecule, where

FT N-(2-aminoethyl)glycine units are linked to

ET nucleotide bases via glycine amino N through a

FT methylenecarbonyl linker"

XX

XX US6046307-A.

XX

PD 04-APR-2000.

XX

XX 09-APR-1997; 97US-0838545.

XX

PR 09-APR-1996; 96US-0630019.

XX

PA (TEXA) UNIV TEXAS SYSTEM.

XX

PI Wright WE, Piatyszek MA, Shay JW, Norton JC, Corey DR;

XX

DR WPI; 2000-292432/25.

XX

PT New peptide nucleic acid (PNA) compounds that inhibit telomerase

PT activity in mammalian cells is useful as probes to detect the RNA

PT component of a mammalian telomerase

XX

XX Example 2; Column 33; 45pp; English.

XX

CC The present sequence represents a peptide nucleic acid molecule which

CC hybridises to the mRNA component of mammalian telomerase, and inhibits

CC telomerase activity. Telomerase is a ribonucleoprotein enzyme that

CC synthesizes one strand of the telomeric DNA, using as a template an 11

CC nucleotide sequence contained within the RNA component of the enzyme. The

CC invention relates to PNA molecules having a sequence of no more than 25

CC bases, which include the sequence GTTAGG. The uncharged nature of the PNA

CC backbone increases the melting temperature of associating strands,

CC increases the rate of association with targeted nucleic acids, and

CC affords greater resistance of degradation by proteases or nucleases. The

CC therapeutic PNAs may be used for treating disease conditions such as

CC cancers, neoplasia, hyperplasia, neurodegenerative diseases, aging, human

CC immunodeficiency virus (HIV) infection/AIDS (acquired immunodeficiency

CC syndrome) and associated pathologies, fungal infections, and other

CC diseases characterized by abnormal telomere metabolism or telomerase

CC activity, in combination with antineoplastic and other cytotoxic or

CC cytostatic agents, antifungal agents, and other nucleotides. PNAs may be

CC used for molecular diagnostics, labelled PNAs are used as hybridization

CC probes to detect or quantitate polynucleotides having a human telomerase

CC RNA (hTR) sequence. PNA probes are also used for forensic identification

CC of individuals, e.g. paternity testing, based on hTR gene restriction

CC fragment length polymorphism (RFLP) pattern. PNAs are also useful as

CC probes to detect the RNA component of a mammalian telomerase and as

CC inhibitors of telomerase activity. The method of the present invention

CC allows cancerous conditions to be detected with increased confidence and

CC possibly at an earlier stage, before cells are detected as cancerous

CC based on pathological characteristics. The diagnostic and prognostic

CC methods of the present invention can be used to detect an immortal or

CC neoplastic cell or tumour tissue or cancer of any origin, provided the

CC cell expresses telomerase activity and its RNA component.

XX

XX Sequence 11 BP; 4 A; 5 C; 0 G; 2 T; 0 other;

XX

Query Match 100.0%; Score 11; DB 21; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.7e+03;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTAACCCCTAAC 11

DB 1 CTAACCCCTAAC 11

RESULT 9

AAA37586/C

ID AAA37586 standard; DNA; 11 BP.

XX

XX AAA37586;

XX

XX 15-AUG-2000 (first entry)

XX

DE Antisense sequence #44 used to inhibit telomerase activity.

KW Peptide nucleic acid; PNA; telomerase; ribonucleoprotein enzyme; cancer;

KW inhibitor; neoplasia; neurodegenerative disease; aging; hyperplasia;

KW AIDS; HIV; fungal infection; forensic identification; detect; tumour;

KW paternity testing; ss.

OS Synthetic.

XX Key Location/Qualifiers

FT misc_feature 1..11

FT /*tag= a

FT /note= "Phosphorothioate internucleotide linkages"

XX US6046307-A.

XX 04-APR-2000.

XX 09-APR-1997; 97US-0838545.

XX 09-APR-1996; 96US-0630019.

XX (TEXA) UNIV TEXAS SYSTEM.

XX Wright WE, Piatyszek MA, Shay JW, Norton JC, Corey DR;

XX WPI; 2000-292432/25.

XX New peptide nucleic acid (PNA) compounds that inhibit telomerase

PT activity in mammalian cells is useful as probes to detect the RNA

PT component of a mammalian telomerase

XX Example 1; Column 27-28; 45pp; English.

XX The present sequence represents an antisense oligonucleotide used as a

CC control sequence alongside a peptide nucleic acid molecule which

CC hybridises to the mRNA component of mammalian telomerase, and inhibits

CC telomerase activity. Telomerase is a ribonucleoprotein enzyme that

CC synthesizes one strand of the telomeric DNA, using as a template an 11

CC nucleotide sequence contained within the RNA component of the enzyme. The

CC invention relates to PNA molecules having a sequence of no more than 25

CC bases, which include the sequence GTTAGG. The uncharged nature of the PNA

CC backbone increases the melting temperature of associating strands,

CC increases the rate of association with targeted nucleic acids, and

CC affords greater resistance of degradation by proteases or nucleases. The

CC therapeutic PNAs may be used for treating disease conditions such as

CC cancers, neoplasia, hyperplasia, neurodegenerative diseases, aging, human

CC immunodeficiency virus (HIV) infection/AIDS (acquired immunodeficiency

CC syndrome) and associated pathologies, fungal infections, and other

CC diseases characterized by abnormal telomere metabolism or telomerase

CC activity, in combination with antineoplastic and other cytotoxic or

CC cytostatic agents, antifungal agents, and other nucleotides. PNAs may be

CC used for molecular diagnostics, labelled PNAs are used as hybridization

CC probes to detect or quantitate polynucleotides having a human telomerase

CC RNA (hTR) sequence. PNA probes are also used for forensic identification

CC of individuals, e.g. paternity testing, based on hTR gene restriction

CC fragment length polymorphism (RFLP) pattern. PNAs are also useful as

CC probes to detect the RNA component of a mammalian telomerase and as

CC inhibitors of telomerase activity. The method of the present invention

CC allows cancerous conditions to be detected with increased confidence and

CC possibly at an earlier stage, before cells are detected as cancerous

CC based on pathological characteristics. The diagnostic and prognostic

CC methods of the present invention can be used to detect an immortal or

CC neoplastic cell or tumour tissue or cancer of any origin, provided the

CC cell expresses telomerase activity and its RNA component.

XX Sequence 11 BP; 2 A; 0 C; 5 G; 4 T; 0 other;

XX Query Match 100.0%; Score 11; DB 21; Length 11;

XX Best Local Similarity 100.0%; Pred. No. 1.7e+03;

XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTAACCCCTAAC 11

Db 11 CTAACCCCTAAC 1

RESULT 10

AAF81185/c

ID AAF81185 standard; DNA; 11 BP.

XX AAF81185;

AC AAF81185;

XX 30-MAY-2001 (first entry)

DT

XX Oligonucleotide thiophosphoramidate, SEQ ID NO: 1.

DE Thiophosphoramidate oligonucleotide; virucide; cytostatic;

KW immunosuppressive; contraceptive; RNA inhibitor; telomerase inhibitor;

KW antisense therapy; viral infection; cancer; hyperproliferative disorder;

KW autoimmune disorder; ss.

XX Synthetic.

OS

XX WO200118015-A1.

PN

XX 15-MAR-2001.

PD

XX 08-SEP-2000; 2000WO-US24688.

PF

XX 10-SEP-1999; 99US-0153201.

PR

XX 19-OCT-1999; 99US-0160444.

PT

XX (GERO-) GERON CORP.

PA

XX Gryaznov S, Pongracz K, Matray T;

PI

XX WPI; 2001-265967/27.

DR

XX Novel thiophosphoramidate polynucleotide useful for detection of RNA or

PT DNA having a given target sequence, for inhibiting RNA function in a

PT cell, and for treating cancer and viral infection

XX Example 3; Page 39; 68pp; English.

PS

XX The present sequence was synthesised in an example illustrating an

CC invention relating to polynucleotides comprising a non-homopolymetric

CC sequence of nucleoside subunits joined by at least one inter-subunit

CC linkage that is a 3'-P5' thiophosphoramidate. The thiophosphoramidate

CC oligonucleotides retain a high RNA binding affinity and exhibit a much

CC higher acid stability. They are useful for detecting a specific sequence

CC in a sample, by forming a hybridisation complex with the sequence. They

CC are useful for inhibiting function of an RNA in a cell (for inhibiting

CC translation of a mRNA or for inhibiting telomerase enzyme in a cell).

CC They are also useful in the preparation of a medicament for treatment of

CC viral infection or cancer. The oligonucleotides are useful for anti-sense

CC and anti-gene diagnostic or therapeutic applications and may be used for

CC treating telomerase-mediated conditions or diseases, such as

CC hyperproliferative and autoimmune disorders, and for contraceptive

CC purposes.

XX Sequence 11 BP; 2 A; 0 C; 5 G; 4 T; 0 other;

XX Query Match 100.0%; Score 11; DB 22; Length 11;

XX Best Local Similarity 100.0%; Pred. No. 1.7e+03;

XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTAACCCCTAAC 11

Db 11 CTAACCCCTAAC 1

RESULT 11

AAH26728/c

ID AAH26728 standard; DNA; 11 BP.

XX

AC AAH26728;
XX
DT 26-NOV-2001 (first entry)
XX
DE Phosphoramidate-linked 2'-arabino-fluorooligonucleotide.
XX
KW 2'-arabino-fluorooligonucleotide; phosphoramidate; telomerase;
KW inhibitor; infection; cancer; diagnosis; therapy; cytostatic;
KW virucide; antisense; antigene; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 2..11 /*tag= a "OTHER"
FT /mod_base= "2'-arabino-fluoronucleosides"
FT modified_base 2..11 /*tag= b
FT /mod_base= "OTHER"
FT /note= "phosphoramidate linkage"
XX
PN WO200153307-A1.
XX
XX 26-JUL-2001.
XX
XX 19-JAN-2001; 2001WO-US01918.
XX
XX 21-JAN-2000; 2000US-178248P.
XX (GERO-) GERON CORP.
XX
PI Gryaznov S, Schultz RG;
XX
XX WPI; 2001-589652/66.
XX
XX Polynucleotides, used to detect and isolate nucleic acids, inhibit
PT function of RNA and telomerase enzymes and to treat e.g. viral
PT infections, contain 2'-arabino-fluoronucleoside(s) linked to
PT nucleoside(s) -
XX
XX Example 6; Page 46; 61pp; English.
XX
XX The present sequence is that of a N3'-P5' 2'-arabino-fluoro
CC phosphoramidate oligonucleotide that is complementary to
CC telomerase RNA. The oligonucleotide was used to assess the
CC relative efficacy of novel 2'-arabino-fluoro phosphoramidate
CC oligonucleotides and their 2'-ribo fluorooligonucleotide
CC counterparts (see AAH26728-35) for the inhibition of telomerase
CC activity. Novel phosphoramidate 2'-arabino-fluorooligonucleotides
CC are generally more acid stable, more resistant to cellular
CC proteases, and also show greater telomerase inhibition activity
CC than 2'-ribose-fluoro phosphoramidates. They are therefore useful
CC for treating cancer (claimed) and other diseases in which telomerase
CC activity is present at abnormal levels, such as hyperproliferative
CC or autoimmune diseases e.g. psoriasis, rheumatoid arthritis,
CC immune system disorders requiring immunosuppression, and in the
CC treatment of viral infection (claimed).
XX
SQ Sequence 11 BP; 2 A; 0 C; 5 G; 4 T; 0 other;
Query Match 100.0%; Score 11; DB 22; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTAACCCCTAAC 11
Db 11 CTAACCCCTAAC 1

RESULT 12
AAH26732/c
ID AAH26732 standard; DNA; 11 BP.

XX
AC AAH26732;
XX
DT 26-NOV-2001 (first entry)
XX
DE Phosphoramidate-linked 2'-ribose-fluorooligonucleotide.
XX
KW 2'-ribose-fluorooligonucleotide; phosphoramidate; telomerase;
KW inhibitor; infection; cancer; diagnosis; therapy; cytostatic;
KW virucide; antisense; antigene; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 2..11 /*tag= a "OTHER"
FT /mod_base= "2'-ribose-fluoronucleosides"
FT modified_base 2..11 /*tag= b
FT /mod_base= "OTHER"
FT /note= "phosphoramidate linkage"
XX
PN WO200153307-A1.
XX
XX 26-JUL-2001.
XX
XX 19-JAN-2001; 2001WO-US01918.
XX
XX 21-JAN-2000; 2000US-178248P.
XX (GERO-) GERON CORP.
XX
PI Gryaznov S, Schultz RG;
XX
XX WPI; 2001-589652/66.
XX
XX Polynucleotides, used to detect and isolate nucleic acids, inhibit
PT function of RNA and telomerase enzymes and to treat e.g. viral
PT infections, contain 2'-arabino-fluoronucleoside(s) linked to
PT nucleoside(s) -
XX
XX Example 6; Page 46; 61pp; English.
XX
XX The present sequence is that of a 2'-ribose-fluoro
CC phosphoramidate oligonucleotide that is complementary to
CC telomerase RNA. The oligonucleotide was used to assess the
CC relative efficacy of novel 2'-arabino-fluoro phosphoramidate
CC oligonucleotides and their 2'-ribose fluorooligonucleotide
CC counterparts (see AAH26728-35) for the inhibition of telomerase
CC activity. Novel phosphoramidate 2'-arabino-fluorooligonucleotides
CC are generally more acid stable, more resistant to cellular
CC proteases, and also show greater telomerase inhibition activity
CC than 2'-ribose-fluoro phosphoramidates. They are therefore useful
CC for treating cancer (claimed) and other diseases in which telomerase
CC activity is present at abnormal levels, such as hyperproliferative
CC or autoimmune diseases e.g. psoriasis, rheumatoid arthritis,
CC immune system disorders requiring immunosuppression, and in the
CC treatment of viral infection (claimed).
XX
SQ Sequence 11 BP; 2 A; 0 C; 5 G; 4 T; 0 other;
Query Match 100.0%; Score 11; DB 22; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTAACCCCTAAC 11
Db 11 CTAACCCCTAAC 1

RESULT 13
AAS14909/c

ID XX AAS14909 standard; DNA; 11 BP.
AC XX AAS14909;
DT 14-FEB-2002 (first entry)
XX
DE Melanogenesis associated oligonucleotide #5.
XX
KW Melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53;
KW anti-inflammatory; dermatological; ophthalmological; anti-psoriatic;
KW immunosuppressive; DNA repair; proliferation inhibitor; apoptosis;
KW tumour necrosis factor inhibitor; photoaging; hyperproliferative disease;
KW carcinoma; oxidative stress; skin cancer; allergy mediated inflammation;
KW conjunctivitis; allergic rhinitis; vitiligo; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1
FT /*tag= a
FT /mod_base= g
FT /note= "Optionally phosphorylated"
FT 1..11
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Optionally phosphorothiolate linkages"
XX
PN WO200174342-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US10162.
XX
PR 31-MAR-2000; 2000US-0540843.
XX
PA (UYBO-) UNIV BOSTON.
XX
PI Gilchrist BA, Yaar M, Eller M;
XX WPI; 2001-626338/72.
XX
DR Inhibiting proliferation of epithelial cells, useful e.g. for treating
XX carcinoma, using specific oligonucleotides that mimic the effects of
PT ultra-violet light
PT
XX
PS Claim 1; Page 37; 74pp; English.
XX
CC The invention describes inhibition of mammalian epithelial cell
CC proliferation by treating cells with at least one oligonucleotide, or
CC its fragment. The compounds, which have cytostatic, anti-allergic,
CC anti-inflammatory, dermatological, ophthalmological, anti-psoriatic and
CC immunosuppressive activities, function as 'ultra-violet mimics' to induce
CC DNA repair processes (or a protective response to later exposure to
CC radiation or chemicals), as a proliferation inhibitor, apoptosis inducer
CC or a tumour necrosis factor inhibitor. Probably they mimic products of
CC DNA damage, or processed DNA-damage intermediates, by inducing the p53
CC pathway, resulting in transient arrest of cell growth, allowing more time
CC for DNA repair to occur before cell division takes place. The method is
CC especially used to treat carcinoma but may also be used to: treat other
CC hyperproliferative states (e.g. psoriasis or precancerous conditions);
CC reduce photoaging, oxidative stress or damage; prevent skin cancer; treat
CC allergically mediated inflammation (atopic or contact dermatitis,
CC allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in
CC cells caused by radiation or chemicals; increase melanin production
CC (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to
CC promote apoptosis in epithelial cells that contain damaged DNA. Also
CC oligonucleotides that contain non-hydrolyzable backbones are used to
CC inhibit apoptosis, in response to DNA damage, in epithelial cell. This
CC sequence is melanogenesis associated oligonucleotide #5. Representative
CC of the telomere over-hang sequence and one of the oligonucleotides used
CC to inhibit mammalian epithelial cell proliferation, described in the
CC method of the invention.

SQ Sequence 11 BP; 2 A; 0 C; 5 G; 4 T; 0 other;
Query Match 100.0%; Score 11; DB 23; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTAACCCCTAAC 11
Db 11 CTAACCCCTAAC 1
RESULT 14
AAS14913
ID AAS14913 standard; DNA; 11 BP.
XX
AC AAS14913;
XX
DT 14-FEB-2002 (first entry)
XX
DE Melanogenesis associated oligonucleotide #9.
XX
KW Melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53;
KW anti-inflammatory; dermatological; ophthalmological; anti-psoriatic;
KW immunosuppressive; DNA repair; proliferation inhibitor; apoptosis;
KW tumour necrosis factor inhibitor; photoaging; hyperproliferative disease;
KW carcinoma; oxidative stress; skin cancer; allergy mediated inflammation;
KW conjunctivitis; allergic rhinitis; vitiligo; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1
FT /*tag= a
FT /mod_base= c
FT /note= "Phosphorylated"
XX
PN WO200174342-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US10162.
XX
PR 31-MAR-2000; 2000US-0540843.
XX
PA (UYBO-) UNIV BOSTON.
XX
PI Gilchrist BA, Yaar M, Eller M;
XX WPI; 2001-626338/72.
XX
DR Inhibiting proliferation of epithelial cells, useful e.g. for treating
XX carcinoma, using specific oligonucleotides that mimic the effects of
PT ultra-violet light
PT
XX
PS Example 12; Page 37; 74pp; English.
XX
CC The invention describes inhibition of mammalian epithelial cell
CC proliferation by treating cells with at least one oligonucleotide, or
CC its fragment. The compounds, which have cytostatic, anti-allergic,
CC anti-inflammatory, dermatological, ophthalmological, anti-psoriatic and
CC immunosuppressive activities, function as 'ultra-violet mimics' to induce
CC DNA repair processes (or a protective response to later exposure to
CC radiation or chemicals), as a proliferation inhibitor, apoptosis inducer
CC or a tumour necrosis factor inhibitor. Probably they mimic products of
CC DNA damage, or processed DNA-damage intermediates, by inducing the p53
CC pathway, resulting in transient arrest of cell growth, allowing more time
CC for DNA repair to occur before cell division takes place. The method is
CC especially used to treat carcinoma but may also be used to: treat other
CC hyperproliferative states (e.g. psoriasis or precancerous conditions);
CC reduce photoaging, oxidative stress or damage; prevent skin cancer; treat
CC allergically mediated inflammation (atopic or contact dermatitis,
CC allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in
CC cells caused by radiation or chemicals; increase melanin production

CC (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to
 CC promote apoptosis in epithelial cells that contain damaged DNA. Also
 CC oligonucleotides that contain non-hydrolyzable backbones are used to
 CC inhibit apoptosis, in response to DNA damage, in epithelial cell. This
 CC sequence is melanogenesis associated oligonucleotide #9, one of the
 CC oligonucleotides used to inhibit mammalian epithelial cell proliferation,
 CC described in the method of the invention.

XX SQ Sequence 11 BP; 4 A; 5 C; 0 G; 2 T; 0 other;

Query Match 100.0%; Score 11; DB 23; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTAAACCCCTAAC 11

Db 1 CTAAACCCCTAAC 11

RESULT 15

AAS15434/c

ID AAS15434 standard; DNA; 11 BP.

XX AC AAS15434;

XX 14-FEB-2002 (first entry)

XX PNA 7/IV inhibiting human and mammalian telomerase activity.

XX Mammalian; peptide nucleic acid; probe; forensic; paternity testing;
 KW human telomerase RNA component; hTR gene RFLP pattern; cancer;
 KW inflammation; lymphoproliferative disease; autoimmune disease;
 KW neurodegenerative disease; neoplasia; hyperplasia; HIV; AIDS;
 KW human immunodeficiency virus; acquired immunodeficiency syndrome;
 KW telomere metabolism; mutant; cytostatic; anti-inflammatory;
 KW immunosuppressive; polyamide backbone; ss.

XX Homo sapiens.

OS Synthetic.

XX FH Key Location/Qualifiers

FT modified_base 1..11

FT /*tag= a

FT /note= "This sequence is a peptide nucleic acid, i.e. it
 contains a polyamide backbone instead of a
 deoxyribose backbone"

XX PN US6294650-B1.

XX PD 25-SEP-2001.

XX PF 08-JUL-1999; 99US-0349532.

XX PR 09-APR-1997; 97US-0838545.

XX PR 09-APR-1996; 96US-0630019.

XX PA (TEXA) UNIV TEXAS SYSTEM.

XX PI Shay JW, Wright WE, Piatyszek MA, Corey DR, Norton JC;

XX DR WPI; 2001-638024/73.

XX New peptide nucleic acids that hybridizes to the RNA component of
 PT mammalian telomerase, useful for treating or preventing cancer,
 PT inflammation, lymphoproliferative diseases, autoimmune disease, or
 PT neurodegenerative diseases

XX PS Claim 7; Column 73; 46pp; English.

XX The present invention relates to peptide nucleic acids (PNAs), comprising
 CC a sequence of 6-25 nucleobases, that inhibit telomerase activity in
 CC mammalian cells by hybridising to the RNA component of mammalian
 CC telomerase. The PNAs are useful as probes to detect the RNA component

CC of mammalian telomerase and as inhibitors of telomerase activity, or to
 CC detect and/or quantitate polynucleotide having the human telomerase
 CC RNA component (hTR) sequence, as well as in forensic identification of
 CC individuals, such as paternity testing or identification of criminal
 CC suspects or unknown descendants based on the hTR gene RFLP pattern. The
 CC PNA can be further used for treating or preventing cancer, inflammation,
 CC lymphoproliferative diseases, autoimmune disease, or neurodegenerative
 CC diseases. The PNAs in combination with other pharmaceuticals (such as
 CC antineoplastic or cytostatic agents) can be used for treating neoplasia,
 CC hyperplasia, human immunodeficiency virus (HIV) infections, acquired
 CC immunodeficiency syndrome (AIDS) and associated pathologies, and other
 CC diseases characterised by abnormal telomere metabolism or telomerase
 CC activity. The present sequence represents one of the PNA sequences
 CC of the invention.

XX SQ Sequence 11 BP; 2 A; 0 C; 5 G; 4 T; 0 other;

Query Match 100.0%; Score 11; DB 23; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.7e+03;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTAAACCCCTAAC 11

Db 11 CTAAACCCCTAAC 1

Search completed: July 6, 2003, 08:07:22

Job time : 244.821 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 6, 2003, 07:52:05 ; Search time 56.9643 seconds
(without alignments)
59.220 Million cell updates/sec

Title: US-09-540-843-9
Perfect score: 11
Sequence: 1 ctaaccctaac 11

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 558892

Minimum DB seq length: 0
Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_NA: *
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3: /cgn2.6/ptodata/1/ina/6A_COMB.seq: *
4: /cgn2.6/ptodata/1/ina/6B_COMB.seq: *
5: /cgn2.6/ptodata/1/ina/PTC05_COMB.seq: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	11	100.0	11	1	US-08-330-123A-2
2	11	100.0	11	1	US-08-482-115B-2
3	11	100.0	11	2	US-08-660-678A-2
c 4	11	100.0	11	2	US-08-531-743-11
5	11	100.0	11	2	US-08-531-743-12
6	11	100.0	11	2	US-08-485-778-36
7	11	100.0	11	2	US-08-472-802C-3
8	11	100.0	11	3	US-08-520-550A-36
c 9	11	100.0	11	3	US-08-630-019A-9
10	11	100.0	11	3	US-08-630-019A-30
c 11	11	100.0	11	3	US-08-630-019A-39
c 12	11	100.0	11	3	US-08-838-545-13
c 13	11	100.0	11	3	US-08-838-545-31
c 14	11	100.0	11	3	US-08-838-545-44
15	11	100.0	11	3	US-08-998-443-2
16	11	100.0	11	4	US-09-060-523-2
c 17	11	100.0	11	4	US-09-349-532-13
c 18	11	100.0	11	4	US-09-349-532-31
c 19	11	100.0	11	4	US-09-349-532-44
20	11	100.0	11	4	US-09-580-517-2
c 21	11	100.0	12	3	US-08-630-019A-10
c 22	11	100.0	12	3	US-08-838-545-8
c 23	11	100.0	12	4	US-09-349-532-8
c 24	11	100.0	13	3	US-08-630-019A-11
c 25	11	100.0	13	3	US-08-630-019A-15
c 26	11	100.0	13	3	US-08-838-545-1
c 27	11	100.0	13	3	US-08-838-545-12

c 28	11	100.0	13	4	US-09-349-532-1	Sequence 1, Appli
c 29	11	100.0	13	4	US-09-349-532-12	Sequence 12, Appli
c 30	11	100.0	15	2	US-08-531-743-4	Sequence 4, Appli
c 31	11	100.0	15	3	US-08-630-019A-12	Sequence 12, Appli
c 32	11	100.0	15	3	US-08-630-019A-18	Sequence 18, Appli
c 33	11	100.0	15	3	US-08-630-019A-40	Sequence 40, Appli
c 34	11	100.0	15	3	US-08-838-545-2	Sequence 2, Appli
c 35	11	100.0	15	3	US-08-838-545-5	Sequence 5, Appli
c 36	11	100.0	15	3	US-08-838-545-45	Sequence 45, Appli
c 37	11	100.0	15	4	US-09-349-532-2	Sequence 2, Appli
c 38	11	100.0	15	4	US-09-349-532-5	Sequence 5, Appli
c 39	11	100.0	15	4	US-09-349-532-45	Sequence 45, Appli
c 40	11	100.0	16	1	US-08-153-051B-11	Sequence 11, Appli
c 41	11	100.0	16	2	US-08-151-477A-11	Sequence 11, Appli
c 42	11	100.0	16	3	US-08-819-867-20	Sequence 20, Appli
c 43	11	100.0	16	4	US-08-464-011B-60	Sequence 60, Appli
c 44	11	100.0	17	2	US-08-531-743-13	Sequence 13, Appli
c 45	11	100.0	17	4	US-08-857-721-12	Sequence 12, Appli

ALIGNMENTS

RESULT 1
US-08-330-123A-2
; Sequence 2, Application US/08330123A
; Patent No. 5583016
; GENERAL INFORMATION:
; APPLICANT: VILLEPONTEAU, Bryant
; APPLICANT: FENG, Junli
; APPLICANT: FUNK, Walter
; APPLICANT: ANDREWS, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/330,123A
; FILING DATE: 27-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15389-000810
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
; US-08-330-123A-2

Query Match 100.0%; Score 11; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.1e+02;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTAACCCCTAAC 11
Db 1 CUAACCCCUAAC 11

RESULT 2
US-08-482-115B-2
; Sequence 2, Application US/08482115B
; Patent No. 5776679
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Assays for the RNA Component of Human
; TITLE OF INVENTION: Telomerase
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US/08/482.115B
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000830US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
US-08-482-115B-2

Query Match 100.0%; Score 11; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.le+02;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTAACCCCTAAC 11
Db 1 CUAACCCCUAAC 11

RESULT 3
US-08-660-678A-2
; Sequence 2, Application US/08660678A
; Patent No. 5837857
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.

; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660.678A
; FILING DATE: 05-JUN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000811US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
US-08-660-678A-2

Query Match 100.0%; Score 11; DB 2; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.le+02;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTAACCCCTAAC 11
Db 1 CUAACCCCUAAC 11

RESULT 4
US-08-531-743-11/c
; Sequence 11, Application US/08531743
; Patent No. 5856096
; GENERAL INFORMATION:
; APPLICANT: Windle, Bradford E.
; APPLICANT: Qiu, Ming
; APPLICANT: Chen, Shi-fong
; APPLICANT: Fletcher, Terace M.
; APPLICANT: Maine, Ira
; TITLE OF INVENTION: Rapid and Sensitive Assays for Detecting and
; TITLE OF INVENTION: Distinguishing Between Processive and
; TITLE OF INVENTION: No. 5856096-Processive Telomerase Activities
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/531,743
FILING DATE: 20-SEP-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: CTCR:026/HVL
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-531-743-11

Query Match 100.0%; Score 11; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTAACCCCTAAC 11
11 CTAACCCCTAAC 1

RESULT 5

US-08-531-743-12
Sequence 12, Application US/08531743
Patent No. 5856096
GENERAL INFORMATION:
APPLICANT: Windle, Bradford E.
APPLICANT: Qiu, Ming
APPLICANT: Chen, Shi-fong
APPLICANT: Fletcher, Terrace M.
APPLICANT: Maine, Ira
TITLE OF INVENTION: Rapid and Sensitive Assays for Detecting and
TITLE OF INVENTION: Distinguishing Between Processive and
TITLE OF INVENTION: No. 5856096-Processive Telomerase Activities
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/531,743
FILING DATE: 20-SEP-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: CTCR:026/HVL
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-531-743-12

Query Match 100.0%; Score 11; DB 2; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.1e+02;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTAACCCCTAAC 11
1 CTAACCCCTAAC 11

RESULT 6

US-08-485-778-36
Sequence 36, Application US/08485778
Patent No. 5876979
GENERAL INFORMATION:
APPLICANT: Andrews, William H.
APPLICANT: Avillion, Ariel Athena
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Greider, Carol
APPLICANT: Marhuenda, Maria Antonia Blasco
APPLICANT: Villeponteau, Bryant
TITLE OF INVENTION: RNA COMPONENT OF TELOMERASE
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: US
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,778
FILING DATE: 07-JE-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/387,524
FILING DATE: 13-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL94-05A4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-485-778-36

Query Match 100.0%; Score 11; DB 2; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.1e+02;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTAACCCCTAAC 11
1 CTAACCCCTAAC 11

RESULT 7
US-08-472-802C-3
; Sequence 3, Application US/08472802C
; Patent No. 5958680
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472.802C
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272.102
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330.123
; FILING DATE: 27-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15389-000820
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0300
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
US-08-472-802C-3

Query Match 100.0%; Score 11; DB 2; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.1e+02;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTAACCCCTAAC 11
I:|||||:|||
Db 1 CUAACCCCUAAC 11

RESULT 8
US-08-520-550A-36
; Sequence 36, Application US/08520550A
; Patent No. 6013468
; GENERAL INFORMATION:
; APPLICANT: Andrews, William H.
; APPLICANT: Avillion, Ariel A.
; APPLICANT: Feng, Junli
; APPLICANT: Greider, Carol
; APPLICANT: Marhuenda, Maria A. B.
; APPLICANT: Villeponteau, Bryant
; TITLE OF INVENTION: RNA Component of Telomerase
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: US
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/520.550A
; FILING DATE: 29-AUG-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/387.524
; FILING DATE: 13-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330.123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272.102
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: CSHL94-05A3B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-520-550A-36

Query Match 100.0%; Score 11; DB 3; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.1e+02;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTAACCCCTAAC 11
I:|||||:|||
Db 1 CUAACCCCUAAC 11

RESULT 9
US-08-630-019A-9/c
; Sequence 9, Application US/08630019A
; Patent No. 6015710
; GENERAL INFORMATION:
; APPLICANT: Shay, Jerry W.
; APPLICANT: Wright, Woodring E.
; APPLICANT: Platzyszek, Mieczyslaw A.
; APPLICANT: Corey, David
; APPLICANT: No. 6015710ton, James C.
; TITLE OF INVENTION: Modulation of Mammalian Telomerase by
; TITLE OF INVENTION: Peptide Nucleic Acids
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30


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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/630,019A
; FILING DATE: 09-JUN-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-0016000US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "peptide nucleic acid (PNA)",
; DESCRIPTION: where (deoxy)ribose-phosphate linkages are replaced by
; DESCRIPTION: N-(2-aminoethyl)glycine units linked to nucleotide bases via
; DESCRIPTION: glycine amino nitrogen through a methylenecarbonyl linker"
; US-08-630-019A-9
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; Query Match 100.0%; Score 11; DB 3; Length 11;
; Best Local Similarity 100.0%; Pred. No. 1.1e+02;
; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; QY 1 CTAACCCCTAAC 11
; Db 11 CTAACCCCTAAC 1
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; RESULT 10
; US-08-630-019A-30
; Sequence 30, Application US/08630019A
; Patent No. 6015710
; GENERAL INFORMATION:
; APPLICANT: Shay, Jerry W.
; APPLICANT: Wright, Woodring E.
; APPLICANT: Piatyszek, Mieczyslaw A.
; APPLICANT: Corey, David
; APPLICANT: No. 6015710ton, James C.
; TITLE OF INVENTION: Modulation of Mammalian Telomerase by
; TITLE OF INVENTION: Peptide Nucleic Acids
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 09-JUN-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-0016000US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "phosphorothioate (PS) nucleic acid"
; US-08-630-019A-39
;
; Query Match 100.0%; Score 11; DB 3; Length 11;
; Best Local Similarity 100.0%; Pred. No. 1.1e+02;
; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; QY 1 CTAACCCCTAAC 11
; Db 11 CTAACCCCTAAC 1
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; RESULT 12
; US-08-838-545-13/c
; Sequence 13, Application US/08838545
; Patent No. 6046307
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
; US-08-630-019A-30
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; Query Match 100.0%; Score 11; DB 3; Length 11;
; Best Local Similarity 81.8%; Pred. No. 1.1e+02;
; Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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; QY 1 CTAACCCCTAAC 11
; Db 1 CUAACCCCUAAC 11
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; RESULT 11
; US-08-630-019A-39/c
; Sequence 39, Application US/08630019A
; Patent No. 6015710
; GENERAL INFORMATION:
; APPLICANT: Shay, Jerry W.
; APPLICANT: Wright, Woodring E.
; APPLICANT: Piatyszek, Mieczyslaw A.
; APPLICANT: Corey, David
; APPLICANT: No. 6015710ton, James C.
; TITLE OF INVENTION: Modulation of Mammalian Telomerase by
; TITLE OF INVENTION: Peptide Nucleic Acids
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 09-JUN-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-0016000US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "phosphorothioate (PS) nucleic acid"
; US-08-630-019A-39
;
; Query Match 100.0%; Score 11; DB 3; Length 11;
; Best Local Similarity 100.0%; Pred. No. 1.1e+02;
; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; QY 1 CTAACCCCTAAC 11
; Db 11 CTAACCCCTAAC 1
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; RESULT 12
; US-08-838-545-13/c
; Sequence 13, Application US/08838545
; Patent No. 6046307
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; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,019
; FILING DATE: 09-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-001610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 44:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "phosphorothioate (PS)
; nucleic acid"
US-08-838-545-44

Query Match 100.0%; Score 11; DB 3; Length 11;
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Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 11 CTAACCCCTAAC 1

RESULT 15

US-08-998-443-2
; Sequence 2, Application US/08998443
; Patent No. 6054575
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/998,443
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/560,678
; FILING DATE: 05-JUN-1996
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000811US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
US-08-998-443-2

Query Match 100.0%; Score 11; DB 3; Length 11;
Best Local Similarity 81.8%; Pred. NO. 1.1e+02;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTAACCCCTAAC 11
111111111111
Db 1 CUAACCCCTAAC 11

Search completed: July 6, 2003, 09:42:20
Job time : 57.9643 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 6, 2003, 08:30:00 ; Search time 120.214 Seconds
(without alignments)
142.836 Million cell updates/sec

Title: US-09-540-843-9
Perfect score: 11
Sequence: 1 ctaaccctaac 11

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1085931 seqs, 780495707 residues

Total number of hits satisfying chosen parameters: 816406

Minimum DB seq length: 0
Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
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c 2	11	100.0	11	9	US-10-122-630-5
c 3	11	100.0	11	9	US-10-122-630-5
c 4	11	100.0	11	9	US-10-122-633-5
c 5	11	100.0	11	9	US-10-122-633-9
c 6	11	100.0	11	10	US-09-057-351-2
c 7	11	100.0	13	9	US-09-893-252-4
c 8	11	100.0	13	9	US-10-038-335-1
c 9	11	100.0	13	9	US-10-038-335-2
c 10	11	100.0	18	8	US-08-463-404-4
c 11	11	100.0	18	8	US-08-463-404-5
c 12	11	100.0	18	9	US-09-893-252-1
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c 20	11	100.0	18	10	US-09-057-351-26
c 21	11	100.0	18	10	US-09-947-659-1
c 22	11	100.0	18	10	US-09-947-659-2
c 23	11	100.0	18	10	US-09-947-659-7
c 24	11	100.0	19	10	US-09-817-387-19
c 25	11	100.0	20	9	US-09-888-326-808
c 26	11	100.0	20	9	US-10-112-653-824
c 27	11	100.0	20	9	US-10-017-995-853
c 28	11	100.0	20	9	US-09-776-479-853
c 29	11	100.0	20	10	US-09-057-351-40
c 30	11	100.0	20	10	US-09-816-248-36
c 31	11	100.0	20	10	US-09-816-248-37
c 32	11	100.0	21	9	US-10-079-500B-1
c 33	11	100.0	21	9	US-10-040-370A-1
c 34	11	100.0	21	10	US-09-817-387-23
c 35	11	100.0	21	10	US-09-817-387-28
c 36	11	100.0	21	10	US-09-801-346-2
c 37	11	100.0	21	10	US-09-923-541-1
c 38	11	100.0	22	9	US-09-940-173A-2
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c 41	11	100.0	22	10	US-09-057-351-41
c 42	11	100.0	22	10	US-09-730-893-2
c 43	11	100.0	22	10	US-09-730-893-8
c 44	11	100.0	23	10	US-09-817-387-14
c 45	11	100.0	23	10	US-09-817-387-16

ALIGNMENTS

RESULT 1
US-09-835-370-63/C
; Sequence 63, Application US/09835370
; Publication No. US20030022172A1
; GENERAL INFORMATION:
; APPLICANT: UHLMANN, EUGEN
; APPLICANT: BREIPOHL, GERHARD
; APPLICANT: WILL, DAVID W
; TITLE OF INVENTION: POLYAMIDE NUCLEIC ACID DERIVATIVES AND AGENTS AND
; FILE OF INVENTION: PROCESSES FOR PREPARING THEM
; FILE REFERENCE: 02481.1742 SEQUENCE LISTING
; CURRENT APPLICATION NUMBER: US/09/835,370
; CURRENT FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 63
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: nucleotide
; OTHER INFORMATION: base sequence of PNA derivatives that bind to
; OTHER INFORMATION: viral and cellular targets
US-09-835-370-63

Query Match 100.0%; Score 11; DB 9; Length 11;
Best Local Similarity 100.0%; Pred.No. 2.6e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTAACCCCTAAC 11
Db 11 CTAACCCCTAAC 1

RESULT 2
US-10-122-630-5/C
; Sequence 5, Application US/10122630
; Publication No. US20030032610A1
; GENERAL INFORMATION:
; APPLICANT: Glitchrest, Barbara A.
; APPLICANT: Eller, Mark S.
; APPLICANT: Yaar, Mina

; TITLE OF INVENTION: Method to Inhibit Cell Growth Using
; FILE OF INVENTION: Oligonucleotides
; FILE REFERENCE: 0054.1088-018
; CURRENT APPLICATION NUMBER: US/10/122,630
; CURRENT FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 08/467,012
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: PCT/US96/08386
; PRIOR FILING DATE: 1996-06-03
; PRIOR APPLICATION NUMBER: US 09/048,927
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: US 09/540,843
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: PCT/US01/10162
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-630-5

Query Match 100.0%; Score 11; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTAACCCCTAAC 11
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Db 11 CTAACCCCTAAC 1

RESULT 3

US-10-122-630-9
; Sequence 9, Application US/10122630
; Publication No. US20030032610A1
; GENERAL INFORMATION:
; APPLICANT: Gilchrist, Barbara A.
; APPLICANT: Eller, Mark S.
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using
; FILE OF INVENTION: Oligonucleotides
; FILE REFERENCE: 0054.1088-018
; CURRENT APPLICATION NUMBER: US/10/122,630
; CURRENT FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 08/467,012
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: PCT/US96/08386
; PRIOR FILING DATE: 1996-06-03
; PRIOR APPLICATION NUMBER: US 09/048,927
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: US 09/540,843
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: PCT/US01/10162
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-630-9

Query Match 100.0%; Score 11; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTAACCCCTAAC 11
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Db 1 CTAACCCCTAAC 11

RESULT 4

US-10-122-633-5/c
; Sequence 5, Application US/10122633
; Publication No. US20030032611A1
; GENERAL INFORMATION:
; APPLICANT: Gilchrist, Barbara A.
; APPLICANT: Eller, Mark S.
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using
; FILE OF INVENTION: Oligonucleotides
; FILE REFERENCE: 0054.1088-019
; CURRENT APPLICATION NUMBER: US/10/122,633
; CURRENT FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 09/540,843
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: PCT/US01/10162
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-633-5

Query Match 100.0%; Score 11; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTAACCCCTAAC 11
|||||

Db 11 CTAACCCCTAAC 1

RESULT 5

US-10-122-633-9
; Sequence 9, Application US/10122633
; Publication No. US20030032611A1
; GENERAL INFORMATION:
; APPLICANT: Gilchrist, Barbara A.
; APPLICANT: Eller, Mark S.
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using
; FILE OF INVENTION: Oligonucleotides
; FILE REFERENCE: 0054.1088-019
; CURRENT APPLICATION NUMBER: US/10/122,633
; CURRENT FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 09/540,843
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: PCT/US01/10162
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-633-9

Query Match 100.0%; Score 11; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTAACCCCTAAC 11
|||||

Db 1 CTAACCCCTAAC 11

RESULT 6
US-09-057-351-2
; Sequence 2, Application US/09057351
; Patent NO. US20010034439A1
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/057,351
; FILING DATE: 08-APR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,802
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000821US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
US-09-057-351-2

Query Match 100.0%; Score 11; DB 10; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.6e+03;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTAACCCCTAAC 11
|:|||||:
Db 1 CUAACCCUAC 11

RESULT 7
US-09-893-252-4/c
; Sequence 4, Application US/09893252
; Publication NO. US20030012755A1
; GENERAL INFORMATION:
; APPLICANT: Styczynski, Peter
; APPLICANT: Ahluwalia, Gurpreet S.
; TITLE OF INVENTION: REDUCTION OF HAIR GROWTH
; FILE REFERENCE: 00216-552001
; CURRENT APPLICATION NUMBER: US/09/893,252

; CURRENT FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-893-252-4

Query Match 100.0%; Score 11; DB 9; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTAACCCCTAAC 11
|:|||||:
Db 13 CTAACCCCTAAC 3

RESULT 8
US-10-038-335-1/c
; Sequence 1, Application US/10038335
; Publication NO. US20030096776A1
; GENERAL INFORMATION:
; APPLICANT: Ecker, David J.
; APPLICANT: Wyatt, Jacqueline
; APPLICANT: Bennett, C. Frank
; APPLICANT: Hanecak, Ronnie
; APPLICANT: Brown-Driver, Vickie
; APPLICANT: Vickers, Timothy
; APPLICANT: Chiang, Ming-yi
; APPLICANT: Anderson, Kevin
; TITLE OF INVENTION: Modulation of Telomere Length By Oligonucleotides Having A G-C
; TITLE OF INVENTION: Sequence
; FILE REFERENCE: ISIS-4976
; CURRENT APPLICATION NUMBER: US/10/038,335
; CURRENT FILING DATE: 2001-01-02
; PRIOR APPLICATION NUMBER: 09/299,058
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: 08/403,888
; PRIOR FILING DATE: 1995-06-12
; PRIOR APPLICATION NUMBER: PCT/US93/09297
; PRIOR FILING DATE: 1993-09-29
; PRIOR APPLICATION NUMBER: 07/954,185
; PRIOR FILING DATE: 1992-09-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 13
; TYPE: DNA
; ORGANISM: No. US20030096776A1el sequence
; FEATURE:
; OTHER INFORMATION: Antisense sequence
US-10-038-335-1

Query Match 100.0%; Score 11; DB 9; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTAACCCCTAAC 11
|:|||||:
Db 13 CTAACCCCTAAC 3

RESULT 9
US-10-038-335-2/c
; Sequence 2, Application US/10038335
; Publication NO. US20030096776A1
; GENERAL INFORMATION:
; APPLICANT: Ecker, David J.
; APPLICANT: Wyatt, Jacqueline
; APPLICANT: Bennett, C. Frank
; APPLICANT: Hanecak, Ronnie
; APPLICANT: Brown-Driver, Vickie

APPLICANT: Vickers, Timothy
APPLICANT: Chiang, Ming-yi
APPLICANT: Anderson, Kevin
TITLE OF INVENTION: Modulation Of Telomere Length By Oligonucleotides Having A G-Core
TITLE OF INVENTION: Sequence
FILE REFERENCE: ISIS-4976
CURRENT APPLICATION NUMBER: US/10/038,335
PRIORITY FILING DATE: 2001-01-02
PRIORITY FILING DATE: 1999-04-23
PRIORITY FILING DATE: 1995-06-12
PRIORITY FILING DATE: 1993-09-29
PRIORITY FILING DATE: 1992-09-29
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 13
TYPE: DNA
ORGANISM: No. US20030096776A1el sequence
FEATURE:
OTHER INFORMATION: Antisense sequence
US-10-038-335-2

Query Match 100.0%; Score 11; DB 9; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTAACCCCTAAC 11
Db 13 CTAACCCCTAAC 3

RESULT 10
US-08-463-404-4
Sequence 4, Application US/08463404
Patent No. US20020127634A1
GENERAL INFORMATION:
APPLICANT: Michael D. West
APPLICANT: Jerry W. Shay
APPLICANT: Woodring E. Wright
APPLICANT: Elizabeth Blackburn
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF CONDITIONS
TITLE OF INVENTION: RELATED TO TELOMERE LENGTH AND/OR
TITLE OF INVENTION: TELOMERASE ACTIVITY
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,404
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/060,952
FILING DATE: May 13, 1993
APPLICATION NUMBER: 07/882,438
FILING DATE: May 13, 1992
APPLICATION NUMBER: 08/038,766
FILING DATE: March 24, 1993

ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 202/045
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 18
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-463-404-4

Query Match 100.0%; Score 11; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTAACCCCTAAC 11
Db 3 CTAACCCCTAAC 13

RESULT 11
US-08-463-404-5/c
Sequence 5, Application US/08463404
Patent No. US20020127634A1
GENERAL INFORMATION:
APPLICANT: Michael D. West
APPLICANT: Jerry W. Shay
APPLICANT: Woodring E. Wright
APPLICANT: Elizabeth Blackburn
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF CONDITIONS
TITLE OF INVENTION: RELATED TO TELOMERE LENGTH AND/OR
TITLE OF INVENTION: TELOMERASE ACTIVITY
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,404
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/060,952
FILING DATE: May 13, 1993
APPLICATION NUMBER: 07/882,438
FILING DATE: May 13, 1992
APPLICATION NUMBER: 08/038,766
FILING DATE: March 24, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 202/045
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:

;
; LENGTH: 18
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-463-404-5

Query Match 100.0%; Score 11; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTAACCCCTAAC 11
Db 16 CTAACCCCTAAC 6

RESULT 12

US-09-893-252-1/c
; Sequence 1, Application US/09893252
; Publication No. US20030012755A1
; GENERAL INFORMATION:
; APPLICANT: Styczynski, Peter
; APPLICANT: Ahluwalia, Gurpreet S.
; TITLE OF INVENTION: REDUCTION OF HAIR GROWTH
; FILE REFERENCE: 00216-552001
; CURRENT APPLICATION NUMBER: US/09/893,252
; CURRENT FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-893-252-1

Query Match 100.0%; Score 11; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTAACCCCTAAC 11
Db 16 CTAACCCCTAAC 6

RESULT 13

US-10-132-002-2
; Sequence 2, Application US/10132002
; Publication No. US20030022204A1
; GENERAL INFORMATION:
; APPLICANT: Lansdorp, Peter
; TITLE OF INVENTION: Method for Detecting Multiple Copies of
; a Repeat Sequence in a Nucleic Acid Molecule
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWSON & HOWSON
; STREET: 321 No. US20030022204A1rlirstown Road
; CITY: Spring House
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/132,002
; FILING DATE: 25-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/730,635
; FILING DATE: 11-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
US-10-132-002-2

;
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: B&P7USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 540-9200
; TELEFAX: (215) 540-5818
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-132-002-2

Query Match 100.0%; Score 11; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTAACCCCTAAC 11
Db 3 CTAACCCCTAAC 13

RESULT 14

US-10-132-002-4/c
; Sequence 4, Application US/10132002
; Publication No. US20030022204A1
; GENERAL INFORMATION:
; APPLICANT: Lansdorp, Peter
; TITLE OF INVENTION: Method for Detecting Multiple Copies of
; a Repeat Sequence in a Nucleic Acid Molecule
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWSON & HOWSON
; STREET: 321 No. US20030022204A1rlirstown Road
; CITY: Spring House
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/132,002
; FILING DATE: 25-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/730,635
; FILING DATE: 11-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: B&P7USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 540-9200
; TELEFAX: (215) 540-5818
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-132-002-4

Query Match 100.0%; Score 11; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CTAACCCCTAAC 11
 Db 16 CTAACCCCTAAC 6

RESULT 15
 US-10-238-732-2
 ; Sequence 2, Application US/10238732
 ; Publication No. US20030077635A1
 ; GENERAL INFORMATION:
 ; APPLICANT: DAKO A/S
 ; TITLE OF INVENTION: DENDRIMERS AND METHODS FOR THEIR PREPARATION AND USE
 ; FILE REFERENCE: P65587US1
 ; CURRENT APPLICATION NUMBER: US/10/238,732
 ; CURRENT FILING DATE: 2002-09-11
 ; PRIOR APPLICATION NUMBER: 09/606,315
 ; PRIOR FILING DATE: 2000-06-29
 ; PRIOR APPLICATION NUMBER: PA 1999 00934
 ; PRIOR FILING DATE: 1999-06-29
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 18
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ; OTHER INFORMATION: linker sequence.
 US-10-238-732-2

Query Match 100.0%; Score 11; DB 9; Length 18;
 Best Local Similarity 100.0%; Pred No. 2.5e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTAACCCCTAAC 11
 Db 6 CTAACCCCTAAC 16

Search completed: July 6, 2003, 12:17:04
 Job time : 121.214 secs

GenCore version 5.1.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 6, 2003, 07:52:05 ; Search time 25.8929 Seconds
(without alignments)
59.220 Million cell updates/sec

Title: US-09-540-843-6

Perfect score: 5

Sequence: 1 catac 5

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 558892

Minimum DB seq length: 0

Maximum DB seq length: 40

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA:*

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2: /cgn2.6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2.6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2.6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2.6/ptodata/1/ina/PTUS_COMB.seq:*
6: /cgn2.6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	5	100.0	5	3	US-08-855-372B-20
C 2	5	100.0	5	3	US-09-048-927-4
C 3	5	100.0	5	4	US-09-498-851-20
C 4	5	100.0	7	1	US-08-615-170-10
C 5	5	100.0	7	1	US-08-615-170-12
C 6	5	100.0	7	3	US-09-048-927-3
C 7	5	100.0	9	2	US-08-583-276-1
C 8	5	100.0	9	3	US-08-646-789A-8
C 9	5	100.0	9	3	US-08-646-789A-80
C 10	5	100.0	9	3	US-09-048-927-1
C 11	5	100.0	9	4	US-09-319-648-68
C 12	5	100.0	10	1	US-08-335-565A-27
C 13	5	100.0	10	1	US-08-250-951-1
C 14	5	100.0	10	1	US-08-232-233-1
C 15	5	100.0	10	1	US-08-222-177A-422
C 16	5	100.0	10	1	US-08-351-748-23
C 17	5	100.0	10	1	US-08-351-748-25
C 18	5	100.0	10	1	US-08-202-927-25
C 19	5	100.0	10	1	US-08-430-536A-23
C 20	5	100.0	10	1	US-08-430-536A-25
C 21	5	100.0	10	1	US-08-171-718-45
C 22	5	100.0	10	2	US-08-703-601-1
C 23	5	100.0	10	2	US-08-684-547-23
C 24	5	100.0	10	2	US-08-684-547-25
C 25	5	100.0	10	3	US-08-469-318-174
C 26	5	100.0	10	3	US-08-468-609A-174
C 27	5	100.0	10	3	US-08-478-087-45

28	5	100.0	10	3	US-09-063-450-24
C 29	5	100.0	10	3	US-09-063-450-33
C 30	5	100.0	10	4	US-09-123-638-1
C 31	5	100.0	10	4	US-08-646-695-30
C 32	5	100.0	10	4	US-08-875-533-31
C 33	5	100.0	10	4	US-08-446-872A-174
C 34	5	100.0	10	4	US-09-724-753-1
C 35	5	100.0	10	4	US-08-762-227A-174
C 36	5	100.0	10	5	PCT-US92-09827-1
C 37	5	100.0	10	5	PCT-US95-01185-174
C 38	5	100.0	10	5	PCT-US95-02419-25
C 39	5	100.0	10	5	PCT-US96-06053-30
C 40	5	100.0	10	6	5198343-3
C 41	5	100.0	11	1	US-08-401-512-19
C 42	5	100.0	11	1	US-08-147-696E-4
C 43	5	100.0	11	1	US-08-696-139-6
C 44	5	100.0	11	1	US-08-484-334-4
C 45	5	100.0	11	2	US-08-441-887A-82

ALIGNMENTS

RESULT 1

US-08-855-372B-20/c
; Sequence 20, Application US/08855372B
; Patent No. 6090549
; GENERAL INFORMATION:
; APPLICANT: Mirzabekov, Andrei D
; APPLICANT: Parinov, Sergei V
; APPLICANT: Barsky, Victor E
; APPLICANT: Kirillov, Eugene V
; APPLICANT: Dubliley, Svetlana A
; TITLE OF INVENTION: Use of Continuous/Contiguous Stacking Hybridization as a Di
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHERSKOV & FLAYNIK
; STREET: 20 N. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.50 inch, 1.4 MB storage
; COMPUTER: PC
; OPERATING SYSTEM: Microsoft Windows 98
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/855,372B
; FILING DATE: 13-MAY-97
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/587,332
; FILING DATE: 16-JAN-96
; ATTORNEY/AGENT INFORMATION:
; NAME: Cherskov, Michael J.
; REGISTRATION NUMBER: 33,664
; REFERENCE/DOCKET NUMBER: ANL-IN-95-027
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 621-1330
; TELEFAX: (312) 621-0088
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 bases
; TYPE: nucleic acid
; STRANDEDNESS: No. 6090549 Applicable
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; HYPOTHETICAL: yes
; US-08-855-372B-20

Query Match 100.0%; Score 5; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 5.8e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 24, Appl
Sequence 33, Appl
Sequence 1, Appl
Sequence 30, Appl
Sequence 31, Appl
Sequence 174, App
Sequence 1, Appl
Sequence 174, App
Sequence 1, Appl
Sequence 174, App
Sequence 25, Appl
Sequence 30, Appl
Patent No. 5198343
Sequence 19, Appl
Sequence 4, Appl
Sequence 6, Appl
Sequence 4, Appl
Sequence 82, Appl

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Qy      1 CATAc 5
       11111
Db      5 CATAc 1

RESULT 2
US-09-048-927-4/c
; Sequence 4, Application US/09048927
; Patent No. 6147056
; GENERAL INFORMATION:
; APPLICANT: Gilchrest, Barbara A.
; APPLICANT: Yaar, Mina
; APPLICANT: Eller, Mark
; TITLE OF INVENTION: Use of Locally Applied DNA Fragments
; FILE REFERENCE: BU94-68A2
; CURRENT APPLICATION NUMBER: US/09/048,927
; CURRENT FILING DATE: 1998-03-26
; EARLIER APPLICATION NUMBER: 08/952,697
; EARLIER FILING DATE: 1996-06-03
; EARLIER APPLICATION NUMBER: 08/467,012
; EARLIER FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 5
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: DNA Fragment
US-09-048-927-4

Query Match      100.0%; Score 5; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 5,8e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CATAc 5
       11111
Db      5 CATAc 1

RESULT 3
US-09-498-851-20/c
; Sequence 20, Application US/09498851
; Patent No. 6440671
; GENERAL INFORMATION:
; APPLICANT: Mirzabekov, Andrei D
; APPLICANT: Parinov, Sergei V
; APPLICANT: Barsky, Victor E
; APPLICANT: Kirillov, Eugene V
; APPLICANT: Dubiley, Svetlana A
; TITLE OF INVENTION: Use of Continuous/Contiguous
; TITLE OF INVENTION: Stacking Hybridization as a Diagnostic Tool.
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHERSKOV & FLAYNIK
; STREET: 20 N. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.50 inch, 1.4 MB storage
; COMPUTER: PC
; OPERATING SYSTEM: Microsoft Windows 98
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/498,851
; FILING DATE:
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: 08/855,372
; FILING DATE: 13-MAY-97
; APPLICATION NUMBER: U.S. 08/587,332

; FILING DATE: 16-JAN-96
; ATTORNEY/AGENT INFORMATION:
; NAME: Cherskov, Michael J.
; REGISTRATION NUMBER: 33,664
; REFERENCE/DOCKET NUMBER: ANL-IN-95-027
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 621-1330
; TELEFAX: (312) 621-0088
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 bases
; TYPE: nucleic acid
; STRANDEDNESS: No. 6440671 Applicable
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; HYPOTHETICAL: yes
US-09-498-851-20

Query Match      100.0%; Score 5; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 5,8e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CATAc 5
       11111
Db      5 CATAc 1

RESULT 4
US-08-615-170-10
; Sequence 10, Application US/08615170
; Patent No. 5776776
; GENERAL INFORMATION:
; APPLICANT: ORDAHL, Charles P.
; APPLICANT: AZAKIE, Anthony
; APPLICANT: WAR, Janet H.
; APPLICANT: FARRANCE, Iain K.G.
; APPLICANT: HALL, Deborah E.
; APPLICANT: STEWART, Alexandre F.R.
; TITLE OF INVENTION: DTEF-1 ISOFORMS AND USES THEREOF
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/615,170
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/01526
; FILING DATE: 06-FEB-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/191,493
; FILING DATE: 04-FEB-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 23070-053120
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 10:
```

```
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..7
; OTHER INFORMATION: /standard_name= "Sph-II binding
; OTHER INFORMATION: site in SV40"
US-08-615-170-10

Query Match          100.0%; Score 5; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CATAc 5
Db      1 CATAc 5
      |||||

RESULT 5
US-08-615-170-12
; Sequence 12, Application US/08615170
; Patent No. 5776776
; GENERAL INFORMATION:
; APPLICANT: ORDAHL, Charles P.
; APPLICANT: AZAKIE, Anthony
; APPLICANT: MAR, Janet H.
; APPLICANT: FARRANCE, Iain K.G.
; APPLICANT: HALL, Deborah E.
; APPLICANT: STEWART, Alexandre F.R.
; APPLICANT: LARKIN, Sarah B.
; TITLE OF INVENTION: DTEF-1 ISOFORMS AND USES THEREOF
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/615,170
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/01526
; FILING DATE: 06-FEB-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/191,493
; FILING DATE: 04-FEB-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 2307U-053120
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..7
; OTHER INFORMATION: /standard_name= "Rat beta-Myosin
; OTHER INFORMATION: Heavy Chain M-CAT binding element "
US-08-615-170-12

Query Match          100.0%; Score 5; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CATAc 5
Db      1 CATAc 5
      |||||

RESULT 6
US-09-048-927-3/c
; Sequence 3, Application US/09048927
; Patent No. 6147056
; GENERAL INFORMATION:
; APPLICANT: Gilchrest, Barbara A.
; APPLICANT: Yaar, Mina
; APPLICANT: Eller, Mark
; TITLE OF INVENTION: Use of Locally Applied DNA Fragments
; FILE REFERENCE: BU94-68A2
; CURRENT APPLICATION NUMBER: US/09/048,927
; CURRENT FILING DATE: 1998-03-26
; EARLIER APPLICATION NUMBER: 08/952,697
; EARLIER FILING DATE: 1996-06-03
; EARLIER APPLICATION NUMBER: 08/467,012
; EARLIER FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 7
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: DNA Fragment
US-09-048-927-3

Query Match          100.0%; Score 5; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CATAc 5
Db      6 CATAc 2
      |||||

RESULT 7
US-08-583-276-1/c
; Sequence 1, Application US/08583276
; Patent No. 5837536
; GENERAL INFORMATION:
; APPLICANT: McDonagh, Kevin T.
; APPLICANT: Nienhuis, Arthur
; APPLICANT: Tolstoshev, Paul
; TITLE OF INVENTION: IMPROVED EXPRESSION OF HUMAN
; TITLE OF INVENTION: MULTIDRUG RESISTANCE GENES AND IMPROVED
; TITLE OF INVENTION: SELECTION OF CELLS TRANSFECTED WITH SUCH GENES
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
; ADDRESSEE: Cecchi & Stewart
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
```

Query Match 100.0%; Score 5; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.2e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: DM4 V2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/583,276
FILING DATE: 05-JAN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/332,444
FILING DATE: 31-OCT-1994
APPLICATION NUMBER: 07/887,712
FILING DATE: 22-MAY-1992
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 bases
TYPE: nucleic acid
STRANDEDNESS: singular
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
DESCRIPTION: Genomic DNA
US-08-583-276-1

Query Match 100.0%; Score 5; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.2e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;
QY 1 CATAc 5
Db 8 CATAc 4

RESULT 8
US-08-646-789A-8/c
Sequence 8, Application US/08646789A
Patent No. 6022863
GENERAL INFORMATION:
APPLICANT: Peyman, John A.
TITLE OF INVENTION: REGULATION OF GENE EXPRESSION
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,789A
FILING DATE: May 21, 1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mistock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6523-006
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-646-789A-8

Query Match 100.0%; Score 5; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.2e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;
QY 1 CATAc 5
Db 5 CATAc 1
RESULT 9
US-08-646-789A-80/c
Sequence 80, Application US/08646789A
Patent No. 6022863
GENERAL INFORMATION:
APPLICANT: Peyman, John A.
TITLE OF INVENTION: REGULATION OF GENE EXPRESSION
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,789A
FILING DATE: May 21, 1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mistock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6523-006
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
US-08-646-789A-80

Query Match 100.0%; Score 5; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.2e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;
QY 1 CATAc 5
Db 5 CATAc 1

RESULT 10
US-09-048-927-1/c
Sequence 1, Application US/09048927
Patent No. 6147056
GENERAL INFORMATION:
APPLICANT: Gilchrist, Barbara A.
APPLICANT: Yaar, Mina
APPLICANT: Eller, Mark
TITLE OF INVENTION: Use of Locally Applied DNA Fragments
FILE REFERENCE: BU94-68A2
CURRENT APPLICATION NUMBER: US/09/048,927
CURRENT FILING DATE: 1998-03-26
EARLIER APPLICATION NUMBER: 08/952,697
EARLIER FILING DATE: 1996-06-03

;; EARLIER APPLICATION NUMBER: 08/467,012
;; EARLIER FILING DATE: 1995-06-06
;; NUMBER OF SEQ ID NOS: 4
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 1
;; LENGTH: 9
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: DNA Fragment
US-09-048-927-1

Query Match 100.0%; Score 5; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.2e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5
Db |||||
7 CATAC 3

RESULT 11
US-09-319-648-68
; Sequence 68, Application US/09319648
; Patent No. 6451530
; GENERAL INFORMATION:
; APPLICANT: Hawkins, Mary
; TITLE OF INVENTION: Fluorescent Nucleotide Analog Hairpin
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/319,648
; FILING DATE: 30-Jul-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/032,844
; FILING DATE: 13-DEC-1996
; APPLICATION NUMBER: WO PCT/US97/22448
; FILING DATE: 10-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Fang, Carol
; REGISTRATION NUMBER: 48,631
; REFERENCE/DOCKET NUMBER: 015280-288100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 68:
US-09-319-648-68

Query Match 100.0%; Score 5; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.2e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5

Db |||||
3 CATAC 7

RESULT 12
US-08-335-565A-27/c
; Sequence 27, Application US/08335565A
; Patent No. 5527671
; GENERAL INFORMATION:
; APPLICANT: Li, Kening
; APPLICANT: Rouse, Douglas I.
; APPLICANT: German, Thomas L.
; TITLE OF INVENTION: ASSAY FOR VERTICILLIUM DAHLIAE
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles and Brady
; STREET: 1 South Pinckney St., PO BOX 2113
; CITY: Madison
; STATE: WI
; COUNTRY: USA
; ZIP: 53701-2113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/335,565A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J
; REGISTRATION NUMBER: 27,386
; REFERENCE/DOCKET NUMBER: 960296.93065
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-251-5000
; TELEFAX: 608-251-9166
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-335-565A-27

Query Match 100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.1e+04;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5
Db |||||
10 CATAC 6

RESULT 13
US-08-250-951-1
; Sequence 1, Application US/08250951
; Patent No. 5532129
; GENERAL INFORMATION:
; APPLICANT: Heller, Michael J
; TITLE OF INVENTION: SELF-ORGANIZING MOLECULAR PHOTONIC
; STRUCTURES BASED ON CHROMOPHORE- AND FLUOROPHORE-CONTAINING
; POLYNUCLEOTIDES AND METHODS OF THEIR USE
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bingham & Fitting
; STREET: 12526 High Bluff Drive, Suite 300
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92130
; COMPUTER READABLE FORM:

```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/250,951
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/790,262
; FILING DATE: 07-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: HEL0002P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-792-3680
; TELEFAX: 619-792-8477
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 10
; OTHER INFORMATION: /note= "Donor chromophore at the 3'
US-08-250-951-1

Query Match 100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.1e+04;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5
Db 4 CATAC 8

RESULT 14
US-08-232-233-1
; Sequence 1, Application US/08232233
; Patent No. 5565322
; GENERAL INFORMATION:
; APPLICANT: Michael J. Heller
; TITLE OF INVENTION: SELF-ORGANIZING MOLECULAR PHOTONIC
; TITLE OF INVENTION: STRUCTURES BASED ON CHROMOPHORE- AND FLUOROPHORE-
; TITLE OF INVENTION: CONTAINING POLYNUCLEOTIDES AND METHODS OF THEIR USE
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
; SOFTWARE: Wordperfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,233
; FILING DATE: May 4, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/790,262
; FILING DATE: NO. 5565322ember 7, 1992
; ATTORNEY/AGENT INFORMATION:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/250,951
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/790,262
; FILING DATE: 07-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: HEL0002P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-792-3680
; TELEFAX: 619-792-8477
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 10
; OTHER INFORMATION: /note= "Donor chromophore at the 3' T nucleotide"
US-08-232-233-1

Query Match 100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.1e+04;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5
Db 4 CATAC 8

RESULT 15
US-08-222-177A-422
; Sequence 422, Application US/08222177A
; Patent No. 5582979
; GENERAL INFORMATION:
; APPLICANT: Weber, James L.
; TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
; TITLE OF INVENTION: (GC-dA)n.(GC-dT)n SEQUENCES AND METHODS OF USING SAME
; NUMBER OF SEQUENCES: 460
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Demitt Ross & Stevens, S.C.
; STREET: 8000 Excelsior Drive, Suite 401
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53717-1914
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/222,177A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/341,562
; FILING DATE: 21-APR-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Sara, Charles S.
; REGISTRATION NUMBER: 30,492
; REFERENCE/DOCKET NUMBER: 09865.601
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 831-2100
; TELEFAX: (608) 831-2106
; TELEX:
; INFORMATION FOR SEQ ID NO: 422:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
```


! MOLECULE TYPE: DNA (genomic)
US-08-222-177A-422

Query Match 100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.1e+04;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAC 5
| | | | |
Db 4 CATAC 8

Search completed: July 6, 2003, 09:42:19
Job time : 27.8929 secs

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OM nucleic - nucleic search, using sw model

Run on: July 6, 2003, 08:30:00 ; Search time 54.6429 Seconds
(without alignments)
142.836 Million cell updates/sec

Title: US-09-540-843-6
Perfect score: 5
Sequence: 1 catac 5

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1085931 seqs, 780495707 residues

Total number of hits satisfying chosen parameters: 816406

Minimum DB seq length: 0
Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_NA.*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq.*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
C 1	5	100.0	5	US-10-122-630-4	Sequence 4, Appli
C 2	5	100.0	5	US-10-122-630-6	Sequence 6, Appli
C 3	5	100.0	5	US-10-122-633-4	Sequence 4, Appli
C 4	5	100.0	5	US-10-122-633-6	Sequence 6, Appli
C 5	5	100.0	7	US-10-122-630-3	Sequence 3, Appli
C 6	5	100.0	7	US-10-122-630-7	Sequence 7, Appli
C 7	5	100.0	7	US-10-122-633-3	Sequence 3, Appli
C 8	5	100.0	7	US-10-122-633-7	Sequence 7, Appli
C 9	5	100.0	8	US-09-142-593-11	Sequence 11, Appl
C 10	5	100.0	8	US-09-927-186-17	Sequence 17, Appl
C 11	5	100.0	8	US-09-861-014-6	Sequence 6, Appli
C 12	5	100.0	9	US-10-122-630-1	Sequence 1, Appli
C 13	5	100.0	9	US-10-122-633-1	Sequence 1, Appli
C 14	5	100.0	9	US-10-096-596-32	Sequence 32, Appl
C 15	5	100.0	9	US-09-990-186-623	Sequence 623, App
C 16	5	100.0	9	US-09-990-186-623	Sequence 2220, Ap
C 17	5	100.0	9	US-09-990-186-2220	Sequence 2256, Ap
C 18	5	100.0	9	US-09-989-994-623	Sequence 623, App
C 19	5	100.0	9	US-09-989-994-2220	Sequence 2220, Ap

ALIGNMENTS

RESULT 1

US-10-122-630-4/c
; Sequence 4, Application US/10122630
; Publication No. US20030032610A1
; GENERAL INFORMATION:
; APPLICANT: Gilchrist, Barbara A.
; APPLICANT: Eller, Mark S.
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using
; TITLE OF INVENTION: Oligonucleotides
; FILE REFERENCE: 0054.1088-018
; CURRENT APPLICATION NUMBER: US/10/122.630
; CURRENT FILING DATE: 2002-04-12
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/467,012
; PRIOR FILING DATE: 1996-06-03
; PRIOR APPLICATION NUMBER: PCT/US96/08386
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: US 09/540,843
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: PCT/US01/10162
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 5
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-630-4

Query Match 100.0%; Score 5; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5

Db 5 CATAC 1

Sequence 2256, Ap
Sequence 623, App
Sequence 2220, Ap
Sequence 2256, Ap
Sequence 5, Appli
Sequence 7, Appli
Sequence 8, Appli
Sequence 622, App
Sequence 636, App
Sequence 1338, Ap
Sequence 1341, Ap
Sequence 1342, Ap
Sequence 1343, Ap
Sequence 622, App
Sequence 636, App
Sequence 1338, Ap
Sequence 1341, Ap
Sequence 1342, Ap
Sequence 1343, Ap
Sequence 16, Appl
Sequence 31, Appl
Sequence 622, App
Sequence 636, App
Sequence 1338, Ap
Sequence 1341, Ap
Sequence 1342, Ap
Sequence 1343, Ap

RESULT 2
US-10-122-630-6
; Sequence 6, Application US/10122630
; Publication No. US20030032610A1
; GENERAL INFORMATION:
; APPLICANT: Gilchrist, Barbara A.
; APPLICANT: Eller, Mark S.
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using
; TITLE OF INVENTION: Oligonucleotides
; FILE REFERENCE: 0054.1088-018
; CURRENT FILING DATE: 2002-04-12
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/467,012
; PRIOR FILING DATE: 1996-06-03
; PRIOR APPLICATION NUMBER: PCT/US96/08386
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: US 09/540,843
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: PCT/US01/10162
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 5
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-630-6

Query Match 100.0%; Score 5; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0;

QY 1 CATAc 5
|||||
Db 1 CATAc 5

RESULT 3
US-10-122-633-4/c
; Sequence 4, Application US/10122633
; Publication No. US20030032611A1
; GENERAL INFORMATION:
; APPLICANT: Gilchrist, Barbara A.
; APPLICANT: Eller, Mark S.
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using
; TITLE OF INVENTION: Oligonucleotides
; FILE REFERENCE: 0054.1088-019
; CURRENT FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 09/540,843
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: PCT/US01/10162
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 5
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-633-4

Query Match 100.0%; Score 5; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0;

QY 1 CATAc 5
|||||
Db 5 CATAc 1

RESULT 4
US-10-122-633-6
; Sequence 6, Application US/10122633
; Publication No. US20030032611A1
; GENERAL INFORMATION:
; APPLICANT: Gilchrist, Barbara A.
; APPLICANT: Eller, Mark S.
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using
; TITLE OF INVENTION: Oligonucleotides
; FILE REFERENCE: 0054.1088-019
; CURRENT FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 09/540,843
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: PCT/US01/10162
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 5
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-633-6

Query Match 100.0%; Score 5; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0;

QY 1 CATAc 5
|||||
Db 1 CATAc 5

RESULT 5
US-10-122-630-3/c
; Sequence 3, Application US/10122630
; Publication No. US20030032610A1
; GENERAL INFORMATION:
; APPLICANT: Gilchrist, Barbara A.
; APPLICANT: Eller, Mark S.
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using
; TITLE OF INVENTION: Oligonucleotides
; FILE REFERENCE: 0054.1088-018
; CURRENT FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 08/467,012
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: PCT/US96/08386
; PRIOR FILING DATE: 1996-06-03
; PRIOR APPLICATION NUMBER: US 09/540,843
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: PCT/US01/10162
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 7
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-630-3

Query Match 100.0%; Score 5; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.2e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAC 5
|
|
|
|
|
Db 6 CATAC 2

RESULT 6

US-10-122-630-7/c
; Sequence 7, Application US/10122630
; Publication No. US20030032610A1
; GENERAL INFORMATION:
; APPLICANT: Gilchrest, Barbara A.
; APPLICANT: Eller, Mark S.
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using
; FILE REFERENCE: 0054.1088-018
; CURRENT APPLICATION NUMBER: US/10/122,630
; CURRENT FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 08/467,012
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: PCT/US96/08386
; PRIOR FILING DATE: 1996-06-03
; PRIOR APPLICATION NUMBER: US 09/048,927
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: US 09/540,843
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: PCT/US01/10162
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 7
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-630-7

Query Match 100.0%; Score 5; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.2e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAC 5
|
|
|
|
|
Db 6 CATAC 2

RESULT 7

US-10-122-633-3/c
; Sequence 3, Application US/10122633
; Publication No. US20030032611A1
; GENERAL INFORMATION:
; APPLICANT: Gilchrest, Barbara A.
; APPLICANT: Eller, Mark S.
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using
; FILE REFERENCE: 0054.1088-019
; CURRENT APPLICATION NUMBER: US/10/122,633
; CURRENT FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 09/540,843
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: PCT/US01/10162
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 7

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-633-3

Query Match 100.0%; Score 5; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.2e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAC 5
|
|
|
|
|
Db 6 CATAC 2

RESULT 8

US-10-122-633-7/c
; Sequence 7, Application US/1012633
; Publication No. US20030032611A1
; GENERAL INFORMATION:
; APPLICANT: Gilchrest, Barbara A.
; APPLICANT: Eller, Mark S.
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using
; FILE REFERENCE: 0054.1088-019
; CURRENT APPLICATION NUMBER: US/10/122,633
; CURRENT FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 09/540,843
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: PCT/US01/10162
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 7
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-633-7

Query Match 100.0%; Score 5; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.2e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAC 5
|
|
|
|
|
Db 6 CATAC 2

RESULT 9

US-09-142-593-11
; Sequence 11, Application US/09142593
; Patent No. US20020016975A1
; GENERAL INFORMATION:
; APPLICANT: HACKETT ET AL.
; TITLE OF INVENTION: DNA-BASED TRANSPOSON SYSTEM FOR THE
; CORRESPONDENCE ADDRESSES: 63
; ADDRESS: MUETING, RAASCH & GEBHARDT, P.A.
; STREET: 119 NORTH FOURTH STREET, SUITE 203
; CITY: MINNEAPOLIS
; STATE: MINNESOTA
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/142,593
FILING DATE: 10-SEP-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/040,664
FILING DATE: 11-MAR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/053,868
FILING DATE: 28-JUL-1997
PRIOR APPLICATION DATA: 60/065,303
FILING DATE: 13-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US98/04687
FILING DATE: 11-MAR-1998
ATTORNEY/AGENT INFORMATION:
NAME: SANDBERG, VICTORIA A.
REGISTRATION NUMBER: 41,287
REFERENCE/DOCKET NUMBER: 110.00450101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1226
TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-142-593-11

Query Match 100.0%; Score 5; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAc 5
Db 2 CATAc 6

RESULT 10
US-09-927-886-17
Sequence 17, Application US/09927886
Patent No. US20020103152A1
GENERAL INFORMATION:
APPLICANT: Kay, Mark A.
APPLICANT: Yant, Stephen
TITLE OF INVENTION: Methods of In Vivo Gene Transfer Using a
TITLE OF INVENTION: Sleeping Beauty Transposon System
FILE REFERENCE: STAN-160CIP
CURRENT APPLICATION NUMBER: US/09/927,886
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/162,279
PRIOR FILING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: 09/440,301
PRIOR FILING DATE: 1999-11-17
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 17
LENGTH: 8
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: transposon repeat sequence
US-09-927-886-17

Query Match 100.0%; Score 5; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAc 5
Db 2 CATAc 6

RESULT 11
US-09-861-014-6
Sequence 6, Application US/09861014
Patent No. US20020115216A1
GENERAL INFORMATION:
APPLICANT: Steer, Clifford
APPLICANT: Kren, Betsy
APPLICANT: Linahan-Stieers, Cheryle
APPLICANT: Mcivor, R.
APPLICANT: Hackett, Perry
TITLE OF INVENTION: Composition for Delivery of Compounds to Cells
FILE REFERENCE: 110.01330101
CURRENT APPLICATION NUMBER: US/09/861,014
CURRENT FILING DATE: 2001-05-19
PRIOR APPLICATION NUMBER: US 60/206,002
PRIOR FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: US 60/285,121
PRIOR FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.0
SEQ ID NO 6
LENGTH: 8
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Direct repeat sequence
US-09-861-014-6

Query Match 100.0%; Score 5; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAc 5
Db 2 CATAc 6

RESULT 12
US-10-122-630-1/c
Sequence 1, Application US/10122630
Publication No. US20030032610A1
GENERAL INFORMATION:
APPLICANT: Gilchrest, Barbara A.
APPLICANT: Yaar, Mina
APPLICANT: Eller, Mark S.
TITLE OF INVENTION: Method to Inhibit Cell Growth Using
TITLE OF INVENTION: Oligonucleotides
FILE REFERENCE: 0054.1088-018
CURRENT APPLICATION NUMBER: US/10/122,630
CURRENT FILING DATE: 2002-04-12
PRIOR APPLICATION NUMBER: US 08/467,012
PRIOR FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: PCT/US96/08386
PRIOR FILING DATE: 1996-06-03
PRIOR APPLICATION NUMBER: US 09/048,927
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: US 09/540,843
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: PCT/US01/10162
PRIOR FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 9
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-630-1

Query Match 100.0%; Score 5; DB 9; Length 9;

```
Best Local Similarity 100.0%; Pred. No. 1.7e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAC 5
Db 7 CATAC 3

RESULT 13
US-10-122-633-1/c
; Sequence 1, Application US/10122633
; Publication NO. US20030032611A1
; GENERAL INFORMATION:
; APPLICANT: Gilchrist, Barbara A.
; APPLICANT: Eller, Mark S.
; APPLICANT: Yaar, Mina
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using
; FILE OF INVENTION: Oligonucleotides
; FILE REFERENCE: 0054.1088-019
; CURRENT APPLICATION NUMBER: US/10/122.633
; CURRENT FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 09/540,843
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: PCT/US01/10162
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-633-1

Query Match 100.0%; Score 5; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAC 5
Db 7 CATAC 3

RESULT 14
US-10-096-596-32
; Sequence 32, Application US/10096596
; Publication NO. US20030049653A1
; GENERAL INFORMATION:
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; APPLICANT: Velculescu, Victor
; APPLICANT: Zhang, Lin
; TITLE OF INVENTION: METHOD FOR SERIAL ANALYSIS OF GENE EXPRESSION
; FILE REFERENCE: 001107.00242
; CURRENT APPLICATION NUMBER: US/10/096,596
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: US 08/527,154
; PRIOR FILING DATE: 1995-09-12
; PRIOR APPLICATION NUMBER: US 08/544,861
; PRIOR FILING DATE: 1995-10-18
; PRIOR APPLICATION NUMBER: US 09/107,228
; PRIOR FILING DATE: 1998-06-30
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-096-596-32

Query Match 100.0%; Score 5; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+08;

US-09-990-186-623
; Sequence 623, Application US/09990186
; Publication NO. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 623
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-990-186-623

Query Match 100.0%; Score 5; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAC 5
Db 2 CATAC 6

Search completed: July 6, 2003, 12:17:03
Job time : 55.6429 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model
Run on: July 6, 2003, 07:33:45 ; Search time 745.536 Seconds
(without alignments)
108.616 Million cell updates/sec

Title: US-09-540-843-6

Perfect score: 5

Sequence: 1 catac 5

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 60474

Minimum DB seq length: 0

Maximum DB seq length: 40

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_esttov:*

6: em_estpl:*

7: em_estro:*

8: em_hic:*

9: gb_estl:*

10: gb_est2:*

11: gb_hic:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_pln:*

21: em_gss_vrt:*

22: em_gss_fun:*

23: em_gss_mam:*

24: em_gss_mus:*

25: em_gss_other:*

26: em_gss_pro:*

27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	5	100.0	14	13	BM398220	BM398220 5009-0-42
2	5	100.0	16	9	AI424037	AI424037 tf51h06.x
3	5	100.0	16	9	AI685758	AI685758 tu37g09.x
4	5	100.0	16	9	AI721735	AI721735 fc31g08.x
5	5	100.0	16	13	BG928185	BG928185 HNC65-1-D
6	5	100.0	17	13	BG929060	BG929060 HNC11-1-G

7	5	100.0	17	14	C21103	C21103 HUMGS000262
8	5	100.0	18	13	BM397954	BM397954 5009-0-39
9	5	100.0	19	9	AA977115	AA977115 Oq24c08.s
10	5	100.0	19	9	AI120725	AI120725 ub72b11.r
11	5	100.0	19	9	AI747751	AI747751 ul21h05.x
12	5	100.0	19	14	C00646	C00646 HUMGS000819
13	5	100.0	19	17	AZ341880	AZ341880 1M007A004
14	5	100.0	19	17	AZ345849	AZ345849 1M0080D16
15	5	100.0	19	17	AZ355195	AZ355195 1M0094G22
16	5	100.0	19	17	AZ406137	AZ406137 1M0175F16
17	5	100.0	19	17	AZ422163	AZ422163 1M0200B22
18	5	100.0	19	17	AZ434551	AZ434551 1M0221C12
19	5	100.0	19	17	AZ464990	AZ464990 1M0274G11
20	5	100.0	19	17	AZ486152	AZ486152 1M0314A04
21	5	100.0	19	17	AZ579566	AZ579566 1M0367L08
22	5	100.0	19	17	AZ614702	AZ614702 1M0443F10
23	5	100.0	19	17	AZ626685	AZ626685 1M0467M01
24	5	100.0	19	17	AZ645469	AZ645469 1M0510L24
25	5	100.0	19	17	AZ647364	AZ647364 1M0513016
26	5	100.0	19	17	AZ759906	AZ759906 1M0553C10
27	5	100.0	19	17	AZ766086	AZ766086 1M0563G19
28	5	100.0	19	17	AZ799396	AZ799396 1M0565N18
29	5	100.0	19	17	AZ815067	AZ815067 1M0568E01
30	5	100.0	19	17	AZ817238	AZ817238 1M0568E01
31	5	100.0	19	17	AZ839614	AZ839614 1M0568E01
32	5	100.0	19	17	AZ864822	AZ864822 1M0568E01
33	5	100.0	19	17	AZ942806	AZ942806 1M0568E01
34	5	100.0	19	17	AZ948421	AZ948421 1M0568E01
35	5	100.0	19	17	AZ948955	AZ948955 1M0568E01
36	5	100.0	19	17	AZ953217	AZ953217 1M0568E01
37	5	100.0	19	17	AZ987324	AZ987324 1M0568E01
38	5	100.0	19	17	AZ990856	AZ990856 1M0568E01
39	5	100.0	20	17	AZ336039	AZ336039 1M0606F09
40	5	100.0	20	17	AZ359199	AZ359199 1M0101M19
41	5	100.0	20	17	AZ369273	AZ369273 1M0119H13
42	5	100.0	20	17	AZ387347	AZ387347 1M0146K12
43	5	100.0	20	17	AZ391065	AZ391065 1M0152H20
44	5	100.0	20	17	AZ398474	AZ398474 1M0163G20
45	5	100.0	20	17	AZ406839	AZ406839 1M0176C16

ALIGNMENTS

RESULT 1
BM398220
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BM398220 14 bp mRNA linear EST 17-JAN-2002
5009-0-42-D11.t.1 Chilcoat/Turkewitz CDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.

BM398220
EST.
Tetrahymena thermophila.

Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.

1 (bases 1 to 14)
Turkewitz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E., Frankel, J. and Klobutcher, L.

EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
Contact: Turkewitz AP

Molecular Genetics and Cell Biology

University of Chicago

920 E. 58th Street, Chicago, IL 60637, USA

Tel: 773 702 4374

Fax: 773 702 3172

Email: apturkew@midway.uchicago.edu

Seq primer: T3.

Location/Qualifiers

1..14

/organism="Tetrahymena thermophila"

/strain="CU428.1"

/db_xref="taxon:5911"
 /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
 /note="Vector: Bluescript2 SK+; Details on library
 preparation can be found in Chilcoat and Turkewitz (2001)
 Proc. Natl. Acad. Sci USA, 98: 8709-8713."

BASE COUNT
 ORIGIN

4 a 5 c 0 g 5 t

Query Match 100.0%; Score 5; DB 13; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.1e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5
 Db 1 CATAC 5

RESULT 2
 AI424037

LOCUS
 DEFINITION
 A1424037 16 bp mRNA linear EST 09-MAR-1999
 tf51h06.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2102843 3'
 similar to TR:Q69566 Q69566 ;, mRNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE

AI424037.1 GI:4269968
 EST.
 human.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 16)
 NCI/WINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

AUTHORS

National Cancer Institute / National Institute of Neurological
 Disorders and Stroke, Brain Tumor Genome Anatomy Project

TITLE

(CGAP/BTGP), Tumor Gene Index
 Unpublished (1998)

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
 Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www.bio.llnl.gov/bbrp/image/image.html

FEATURES
 source

Trace considered overall poor quality
 Seq primer: -40UP from Gibco
 High quality sequence stop: 1.

Location/Qualifiers

1..16
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2102843"
 /clone_lib="NCI_CGAP_Brn23"
 /tissue_type="glioblastoma (pooled)"
 /lab_host="DH10B"
 /note="Organ: brain; Vector: p7T3D-Pac (Pharmacia) with a
 modified polylinker; Site.1: Not I; Site.2: Eco RI; 1st
 strand cDNA was primed with a Not I - oligo(dT) primer [5'
 TGTTCACCATCGAGTGGAGCGCCGCATATCTTTTTTTTTTTTTTTTTTT
 T 3']; double-stranded cDNA was ligated to Eco RI
 adaptors (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of the modified p7T3 vector.
 Library is normalized, and was constructed by Bento
 Soares and M. Fatima Bonaldo."

BASE COUNT
 ORIGIN

8 a 6 c 1 g 1 t

Query Match
 Best Local Similarity 100.0%; Score 5; DB 9; Length 16;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5
 Db 2 CATAC 6

RESULT 3
 AI685758

LOCUS
 DEFINITION

AI685758 16 bp mRNA linear EST 27-MAY-1999
 tu37909.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2253280 3'
 similar to TR:Q02393 Q02393 HUMAN PAPILLOMAVIRUS 18 E5 CENTRAL
 SEQUENCE MOTIF PROTEIN 1 ;contains element LTR4 repetitive element
 ;, mRNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE

AI685758.1 GI:4897052
 EST.
 human.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 16)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

AUTHORS

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index

TITLE

Unpublished (1997)

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.
 DNA Sequencing by: Greg Lennon, Ph.D.

CDNA Library Arrayed by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www.bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
 Seq primer: -40UP from Gibco
 High quality sequence stop: 1.

Location/Qualifiers

1..16
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2253280"
 /clone_lib="NCI_CGAP_Pr28"
 /sex="male"
 /dev_stage="adult"
 /lab_host="DH10B"
 /note="Organ: prostate; Vector: p7T3D-Pac (Pharmacia)
 with a modified polylinker; plasmid DNA from the
 normalized library NCI_CGAP_Pr22 was prepared, and ss
 circles were made in vitro. Following HAP purification,
 this DNA was used as tracer in a subtractive hybridization
 reaction. The driver was PCR-amplified cDNAs from a pool
 of 5,000 clones made from the same library (clones IDs
 985608-986759, 1101192-1101959, and 1217928-1220615).
 Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 7 a 7 c 1 g 1 t

Query Match 100.0%; Score 5; DB 9; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.2e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5
 Db 5 CATAC 9

RESULT 4
 AI721735

LOCUS
 DEFINITION

AI721735 16 bp mRNA linear EST 07-JUN-2001
 rc31908.x1 zebrafish WashU MPIMG EST Danio rerio cDNA clone

IMAGE:3723038 3' similar to SW:YM14_PART2 P15615 HYPOTHETICAL 47.2
 KD PROTEIN ;, mRNA sequence.
 AI721735
 AI721735.1 GI:5040064
 EST.
 SOURCE
 ORGANISM

zebrafish.
 Danio rerio

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
 ; Cyprinidae; Danio.

REFERENCE
 AUTHORS
 1 (bases 1 to 16)
 Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy
 ,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood
 ,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B.,
 Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E.,
 Kohn,S., Shin,T., Jackson,J., Cardenas,M., McCann,R., Waterston,R.
 and Wilson,R.

WashU zebrafish EST Project 1998

Unpublished (1998)

Other ESTs: fc31q08.y1

Contact: Stephen L. Johnson

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: zbrafish@watson.wustl.edu

CDNA Library Preparation: Matthew Clark. cDNA Library Arrayed by:
 Matthew Clark. DNA Sequencing by: Washington University Genome
 Sequencing Center Clone distribution: Genome Systems, St. Louis,
 Missouri (web address: www.genomesystems.com) (email contact:
 info@genomesystems.com) and Research Genetics, Huntsville, Alabama
 (web address: www.resgen.com) (email contact: info@resgen.com) and
 RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
 www.rzpd.de)

Trace considered overall poor quality

Possible reversed clone: similarity on wrong strand

Seq primer: T7 ET from Amersham

High quality sequence stop: 1.

FEATURES
 source

1..16
 /organism="Danio rerio"
 /db_xref="taxon:7955"
 /clone="IMAGE:3723038"
 /clone_lib="zebrafish WashU MPMG EST"
 /sex="mixed"
 /tissue_type="26 somite embryos, adult livers, shield
 stage embryos"
 /lab_host="XLI-blue MRF"
 /note="Vector: pSPORT1; Site_1: NotI; Site_2: SalI; 1st
 strand cDNA was primed with a Not I - oligo(dT)15 primer
 [5'GCAGTACTCTAGATCCGACGCCGCCCTTTTCTTTT3'];
 double-stranded cDNA was ligated to Sal I adaptors (BRL),
 digested with Not I and cloned into the Not I and Sal I
 sites of the pSPORT1 vector (BRL). Library was constructed
 by Matthew Clark (Lehrach lab; ICRF, London and Max Planck
 Institut fuer Molekulare Genetik, Berlin). cDNAs for EST
 analysis were selected following oligonucleotide
 hybridization fingerprinting of arrayed clones from
 zebrafish late somitogenesis (26 ss), adult liver or
 embryonic shield stage (5.6 h) libraries. Fingerprint
 data were used to computationally cluster cDNAs, and a
 single cDNA from each cluster was chosen for sequencing.
 In some cases multiple members of the same cluster were
 sequenced to assess clustering parameters or single clones
 were sequenced additional times to assess quality
 control."

BASE COUNT
 ORIGIN

6 a 8 c 1 g 1 t

Query Match

Best Local Similarity 100.0%; Score 5; DB 9; Length 16;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
 Db

1 CATAC 5
 |||||
 9 CATAC 13

RESULT 5
 BG928185

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

COMMENT

CONTACT: Sanjay Kumar

GlaxoSmithKline

709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA

Tel: 610-270-7245

Fax: 610-270-5598

Email: sanjay_kumar@gsk.com

Seq primer: T7

Location/Qualifiers

1..16

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="HNC (Human Normal Cartilage)"

/tissue_type="cartilage"

/lab_host="E.coli DH10 B"

/note="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI;
 Directional"

BASE COUNT 4 a 6 c 2 g 3 t 1 others

ORIGIN

Query Match 100.0%; Score 5; DB 13; Length 16;

Best Local Similarity 100.0%; Pred. No. 1.2e-06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
 Db

1 CATAC 5
 |||||
 8 CATAC 12

RESULT 6

BG929060

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

IDENTIFICATION AND INITIAL CHARACTERIZATION OF 5000 EXPRESSED
 SEQUENCED TAGS (ESTs) EACH FROM ADULT HUMAN NORMAL AND

EST.

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 17)

Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
 Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
 Lark,M.W.

IDENTIFICATION AND INITIAL CHARACTERIZATION OF 5000 EXPRESSED
 SEQUENCED TAGS (ESTs) EACH FROM ADULT HUMAN NORMAL AND

16 bp mRNA linear EST 06-NOV-2001
 HNC65-1-D12.R.R HNC (Human Normal Cartilage) Homo sapiens CDNA,
 mRNA sequence.

BG928185

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

COMMENT

CONTACT: Sanjay Kumar

GlaxoSmithKline

709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA

Tel: 610-270-7245

Fax: 610-270-5598

Email: sanjay_kumar@gsk.com

Seq primer: T7

Location/Qualifiers

1..16

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="HNC (Human Normal Cartilage)"

/tissue_type="cartilage"

/lab_host="E.coli DH10 B"

/note="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI;
 Directional"

BASE COUNT 4 a 6 c 2 g 3 t 1 others

ORIGIN

Query Match 100.0%; Score 5; DB 13; Length 16;

Best Local Similarity 100.0%; Pred. No. 1.2e-06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
 Db

1 CATAC 5
 |||||
 8 CATAC 12

RESULT 6

BG929060

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

IDENTIFICATION AND INITIAL CHARACTERIZATION OF 5000 EXPRESSED
 SEQUENCED TAGS (ESTs) EACH FROM ADULT HUMAN NORMAL AND

EST.

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 17)

Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
 Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
 Lark,M.W.

IDENTIFICATION AND INITIAL CHARACTERIZATION OF 5000 EXPRESSED
 SEQUENCED TAGS (ESTs) EACH FROM ADULT HUMAN NORMAL AND

JOURNAL
MEDLINE
COMMENT
osteoarthritic cartilage cDNA libraries
Osteoarthr. Cartil. 9 (7), 641-653 (2001)
21482651
Contact: Sanjay Kumar
UW2109
GlaxoSmithKline
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
Tel: 610-270-7245
Fax: 610-270-5598
Email: sanjay_kumar-legsk.com
Seq primer: T7.

FEATURES

source
1. .17
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HNC (Human Normal Cartilage)"
/tissue_type="cartilage"
/lab_host="E.coli DH10 B"
/note="Vector: pSPORT I; Site_1: SalI; Site_2: NotI;
Directional"

BASE COUNT 5 a 8 c 2 g 2 t
ORIGIN
Query Match 100.0%; Score 5; DB 13; Length 17;
Best Local Similarity 100.0%; Pred. NO. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAC 5
Db 6 CATAC 10

RESULT 7

C21103
LOCUS HOMGS0002626 Human adult (K.Okubo) Homo sapiens cDNA 3', mRNA EST 23-OCT-1996
DEFINITION
ACCESSION C21103
VERSION C21103.1 GI:1622213
KEYWORDS EST.
SOURCE human.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 17)

Okubo.K
BodyMap: human gene expression database
Unpublished (1995)

JOURNAL
COMMENT
Contact: Okubo, K.
Institute for Molecular and Cellular Biol
Osaka University
1-3, Yamada-oka, Suita, Osaka Pref. 565, Japan
Tel: 06-877-5111(ex.3315)
Email: kousaku@imcb.osaka-u.ac.jp

Human Gene Signature, 3'-directed cDNA sequence. We are not submitting the same cDNA sequence redundantly to DBJ since 1993. For the abundance information of clones with this sequence in this library and as well as in other 3'-directed libraries, see http://www.imcb.osaka-u.ac.jp/bodymap/. The sequences of the clones represented by this GS sequences is also found there.

FEATURES

source
1. .17
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Human adult (K.Okubo)"
/dev_stage="adult"

/note="Organ: blood; Vector: 1-gt-11; Site_1: Eco-RI;
Monocytes were prepared from blood by ficoll-hypaque,
percoll and T cell rosetting purification steps (purity:
96 %). mRNA was prepared from activated monocytes from a
patient with rheumatoid arthritis. mRNA was reverse
transcribed with MULV. Using Eco-RI linkers cDNA was
cloned into 1-gt-11 vector arms. The cDNA library was

screened by differential hybridization using radioactively
marked ss-cDNA from activated and non-activated
monocytes.

BASE COUNT 5 a 5 c 2 g 5 t
ORIGIN

Query Match 100.0%; Score 5; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. NO. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAC 5
Db 9 CATAC 13

RESULT 8

BM397954
LOCUS 5009-0-39-G08.t.1 Chilcoat/Turkewitz cDNA (large fraction)
DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION BM397954
VERSION BM397954.1 GI:18198022
KEYWORDS EST.
SOURCE Tetrahymena thermophila.
ORGANISM Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
1 (bases 1 to 18)

REFERENCE
AUTHORS Turkewitz,A.P., Karrer,K.N., Jahn,C., Orlas,E., Kirk,K.E., Frankel
J. and Klobutcher,L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

FEATURES
Location/Qualifiers
1. .18
/organism="Tetrahymena thermophila"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

BASE COUNT 3 a 7 c 5 g 3 t
ORIGIN

Query Match 100.0%; Score 5; DB 13; Length 18;
Best Local Similarity 100.0%; Pred. NO. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAC 5
Db 1 CATAC 5

RESULT 9

AA977115/c
LOCUS AA977115
DEFINITION OQ24C08.s1 NCL_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1587278 3',
similar to TR:Q69566 Q69566 ;, mRNA sequence.
ACCESSION AA977115
VERSION AA977115.1 GI:3154561
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1. (bases 1 to 19)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers

FEATURES
source

1..19
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1587278"
/clone_lib="NCI-CGAP_GC4"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from 3 pooled
germ cell tumors, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT7T3
vector. Library is normalized. Library was constructed by
Bento Soares and M. Fatima Bonaldo."

BASE COUNT 2 a 0 c 7 g 10 t
ORIGIN

Query Match 100.0%; Score 5; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAC 5
|||||
Db 13 CATAC 9

RESULT 10
AII120725
LOCUS
DEFINITION

ub72b11.r1 Soares mammary_gland_NMLMG Mus musculus cDNA clone
IMAGE:1383261 5', similar to TR:Q15009 Q15009 ORF, COMPLETE CDS. ; ,
mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AII120725
AII120725.1 GI:3521049
EST.
house mouse.
Mus musculus

REFERENCE
AUTHORS

1 (bases 1 to 19)
Geisel S., Kucaba T., Allen M., Bowles M., Dietrich N., Dubuque T.,
Schellenberg K., Steptoe M., Lacy M., Le M., Martin J., Morris M.,
Theising B., Wylie T., Lennon G., Soares B., Wilson R. and
Waterston R.

TITLE
JOURNAL
COMMENT

The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800

Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:905729
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers

FEATURES
source

1..19
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:1383261"
/clone_lib="Soares_mammary_gland_NMLMG"
/sex="female (lactating)"
/tissue_type="mammary gland"
/lab_host="DH10B"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from mammary
gland tissue from a lactating female, and was then primed
with a Not I - oligo(dT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
modified pT7T3 vector. Library is normalized. Library
was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 9 a 3 c 4 g 3 t
ORIGIN

Query Match 100.0%; Score 5; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAC 5
|||||
Db 7 CATAC 11

RESULT 11
AII747751/c
LOCUS
DEFINITION

u121h05.x1 Sugano mouse embryo mewa Mus musculus cDNA clone
IMAGE:2088249 3', similar to TR:P79101 P79101 CLEAVAGE AND
POLYADENYLATION SPECIFICITY FACTOR PROTEIN. ; , mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AII747751
AII747751.1 GI:5126015
EST.
house mouse.
Mus musculus

REFERENCE
AUTHORS

1 (bases 1 to 19)
Marra M., Hillier L., Kucaba T., Martin J., Beck C., Wylie T.,
Underwood K., Steptoe M., Theising B., Allen M., Bowers Y., Person
B., Swaller T., Gibbons M., Pape D., Harvey N., Schurk R., Ritter
E., Kohn S., Shin T., Jackson Y., Cardenas M., McCann R.,
Waterston R. and Willson R.

TITLE
JOURNAL
COMMENT

Unpublished (1999)
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:995933
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: custom primer used
High quality sequence stop: 1.
Location/Qualifiers

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source
1. .19
/organism="Mus musculus"
/strain="C57BL"
/db_xref="taxon:10090"
/clone_lib="IMAGE:2088249"
/clone_stage="embryo, 14 dpc"
/lab_host="DH10B"
/notes="Vector: pME18S-FL3; Site.1: DraIII (CACTGTGTC);
Site.2: DraIII (CACCATGTG); 1st strand cDNA was primed
with an oligo(dT) primer [ATGCGCCCTTTTCTTTTTTTTTTTT];
double-stranded cDNA was ligated to a DraIII adaptor
[CTGTGGCTACTGG], digested and cloned into distinct DraIII
sites of the pME18S-FL3 vector (5' site CACTGTGTC, 3' site
CACCATGTG). XhoI should be used to isolate the cDNA
insert. Size selection was performed to exclude fragments
<1.5kb. Library constructed by Dr. Sumio Sugano
(University of Tokyo Institute of Medical Science).
Custom primers for sequencing: 5' end primer
CTTCTGCTCTAAAGCTGCG and 3' end primer
CGACCTGCAGCTCGAGCACA." 3 t
BASE COUNT      6 a      2 c      8 g      3 t
ORIGIN

Query Match      100.0%; Score 5; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CATAAC 5
        |||||
Db      17 CATAAC 13

RESULT 12
C00646/c
LOCUS      HUMGS008192 Human adult (K.Okubo) Homo sapiens cDNA, mRNA
DEFINITION
ACCESSION      C00646
VERSION
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS      Okubo,K.
TITLE      BodyMap: human gene expression database
JOURNAL      Unpublished (1995)
COMMENT      Contact: Okubo,K.
Institute for Molecular and Cellular Biol
Osaka University
1-3,Yanada-oka, Suita, Osaka Pref. 565, Japan
Tel: 06-877-5111(ex.3315)
Email: kousaku@imcb.osaka-u.ac.jp
Human Gene Signature, 3'-directed cDNA sequence. We are not
submitting the same cDNA sequence redundantly to DDBJ since 1993.
For the abundance information of clones with this sequence in this
library and as well as in other 3'-directed libraries, see
http://www.imcb.osaka-u.ac.jp/bodymap/. The sequences of the clones
represented by this GS sequences is also found there.

FEATURES
source
1. .19
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Human adult (K.Okubo)"
/dev_stage="adult"
/notes="Organ: blood; Vector: 1-gt-11; Site.1: Eco-RI;
Monocytes were prepared from blood by ficoll-hypaque,
percoll and T cell rosetting purification steps (purity:
96 %). mRNA was prepared from activated monocytes from a
patient with rheumatoid arthritis. mRNA was reverse
transcribed with MuLV. Using Eco-RI linkers cDNA was
cloned into 1-gt-11 vector arms. The cDNA library was
screened by differential hybridization using radioactively
marked ss-cDNA from activated and non-activated
monocytes."
BASE COUNT      4 a      1 c      8 g      6 t
ORIGIN

Query Match      100.0%; Score 5; DB 14; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CATAAC 5
        |||||
Db      18 CATAAC 14

RESULT 13
AZ3411880/c
LOCUS      AZ3411880
DEFINITION      clone UUGC1M0074004 R, DNA sequence.
ACCESSION      AZ3411880
VERSION
KEYWORDS      GSS.
SOURCE      house mouse.
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.
and Wright,D., Weiss,R.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL      Unpublished (2000)
COMMENT      Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0074 row: 0 column: 04
Seq primer: CACACAGGAACACGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
1. .19
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_lib="UUGC1M0074004"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/notes="Vector: FWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (g114732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and

```

Mon Jul- 7 13:08:53 2003

purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 4 a 4 c 6 g 5 t

ORIGIN

Query Match 100.0%; Score 5; DB 17; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5

Db 12 CATAC 8

RESULT 14
AZ345849 19 bp DNA linear GSS 29-SEP-2000
LOCUS
DEFINITION
IM0080D16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0080D16 R, DNA sequence.

ACCESSION
AZ345849

VERSION
AZ345849.1 GI:10425086

KEYWORDS
GSS.

SOURCE
house mouse.

ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0080 row: D column: 16

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

1. 19

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0080D16"

/clone.lib="Mouse 10kb plasmid UUGC1M library"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 9 a 4 c 0 g 6 t

ORIGIN

Query Match 100.0%; Score 5; DB 17; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5

Db 1 CATAC 5

RESULT 15

AZ355195

LOCUS

DEFINITION

IM0094G22R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC1M0094G22 R, DNA sequence.

ACCESSION

AZ355195

VERSION

AZ355195.1 GI:10467355

KEYWORDS

GSS.

SOURCE

house mouse.

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 19)

REFERENCE

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly

M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.

and Wright,D., Weiss,R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0094 row: G column: 22

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

1. 19

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0094G22"

/clone.lib="Mouse 10kb plasmid UUGC1M library"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 7 a 7 c 3 g 2 t
ORIGIN

Query Match 100.0%; Score 5; DB 17; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAc 5
|||||
Db 8 CATAc 12

Search completed: July 6, 2003, 09:39:42
Job time : 750.536 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 6, 2003, 06:42:31 ; Search time 237.5 Seconds
(without alignments)
612.691 Million cell updat

Title: US-09-540-843-6
Perfect score: 5
Sequence: 1 catcac 5

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 774614

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Minimum DB seq length: 0
Maximum DB seq length: 40
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*

- 1: gb_ba.*
- 2: gb_hug.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vl.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_om.*
- 21: em_or.*
- 22: em_ov.*
- 23: em_pat.*
- 24: em_ph.*
- 25: em_pl.*
- 26: em_to.*
- 27: em_sts.*
- 28: em_un.*
- 29: em_vl.*
- 30: em_hug_hum.*
- 31: em_hug_inv.*
- 32: em_hug_other.*
- 33: em_hug_mus.*
- 34: em_hug_pln.*
- 35: em_hug_rod.*
- 36: em_hug_mam.*
- 37: em_hug_vrt.*
- 38: em_sy.*
- 39: em_hugo_hum.*
- 40: em_hugo_mus.*
- 41: em_hugo_other.*

pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query			ID	Description
		Match	Length	DB		
C 1	5	100.0	5	6	AX268756	Sequence
C 2	5	100.0	5	6	AX268758	Sequence
C 3	5	100.0	7	6	AX268735	Sequence
C 4	5	100.0	7	6	AX268759	Sequence
C 5	5	100.0	8	6	AX047565	Sequence
C 6	5	100.0	8	6	AX104946	Sequence
C 7	5	100.0	8	6	AX119567	Sequence
C 8	5	100.0	9	6	AX268753	Sequence
C 9	5	100.0	9	9	S50583	S50583 type I proc
C 10	5	100.0	9	9	S50585	S50585 type I proc
C 11	5	100.0	10	6	A18263	A18263 oligonucle
C 12	5	100.0	10	6	AR065157	Sequence
C 13	5	100.0	10	6	AR079101	Sequence
C 14	5	100.0	10	6	AR079103	Sequence
C 15	5	100.0	10	6	AR098909	Sequence
C 16	5	100.0	10	6	AR107335	Sequence
C 17	5	100.0	10	6	AR107344	Sequence
C 18	5	100.0	10	6	AR123039	Sequence
C 19	5	100.0	10	6	AR136787	Sequence
C 20	5	100.0	10	6	AR160130	Sequence
C 21	5	100.0	10	6	AR202278	Sequence
C 22	5	100.0	10	6	AX080424	Sequence
C 23	5	100.0	10	6	AX104930	Sequence
C 24	5	100.0	10	6	AX112988	Sequence
C 25	5	100.0	10	6	AX112993	Sequence
C 26	5	100.0	10	6	AX113002	Sequence
C 27	5	100.0	10	6	AX152720	Sequence
C 28	5	100.0	10	6	AX152760	Sequence
C 29	5	100.0	10	6	AX152761	Sequence
C 30	5	100.0	10	6	AX153151	Sequence
C 31	5	100.0	10	6	AX153528	Sequence
C 32	5	100.0	10	6	AX153564	Sequence
C 33	5	100.0	10	6	AX153578	Sequence
C 34	5	100.0	10	6	AX153616	Sequence
C 35	5	100.0	10	6	AX252791	Sequence
C 36	5	100.0	10	6	AX252792	Sequence
C 37	5	100.0	10	6	AX252795	Sequence
C 38	5	100.0	10	6	AX252796	Sequence
C 39	5	100.0	10	6	AX252827	Sequence
C 40	5	100.0	10	6	AX252828	Sequence
C 41	5	100.0	10	6	AX252832	Sequence
C 42	5	100.0	10	6	AX252867	Sequence
C 43	5	100.0	10	6	AX252869	Sequence
C 44	5	100.0	10	6	AX252871	Sequence
C 45	5	100.0	10	6	AX252873	Sequence

ALIGNMENTS

[illegible]


```

RESULT 6
AX104946/c
LOCUS AX104946 8 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 1138 from Patent WO0122972.
ACCESSION AX104946
VERSION AX104946.1 GI:13921143
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE
AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 1138 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DB)
FEATURES
source Location/Qualifiers
1..8
/organism="synthetic construct"
/db_xref="taxon:32630"
BASE COUNT 2 a 1 c 2 g 3 t
ORIGIN

Query Match 100.0%; Score 5; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 3.6e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAc 5
Db 7 CATAc 3

RESULT 7
AX119567/c
LOCUS AX119567 8 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 224 from Patent WO0129251.
ACCESSION AX119567
VERSION AX119567.1 GI:14036486
KEYWORDS
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE
AUTHORS Messiaen,L. and Callens,T.
TITLE Improved mutation analysis of the nfl gene
JOURNAL Patent: WO 0129251-A 224 26-APR-2001;
UNIVERSITEIT GENT (BE)
FEATURES
source Location/Qualifiers
1..8
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 1 a 0 c 4 g 3 t
ORIGIN

Query Match 100.0%; Score 5; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 3.6e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAc 5
Db 7 CATAc 3

RESULT 8
AX268753/c
LOCUS AX268753 9 bp DNA linear PAT 29-OCT-2001
DEFINITION Sequence 1 from Patent WO0174342.
ACCESSION AX268753
VERSION AX268753.1 GI:16541825
KEYWORDS
SOURCE synthetic construct.

```

```

ORGANISM synthetic construct
artificial sequences.
REFERENCE
AUTHORS Gilchrest,B.A., Yaar,M. and Eller,M.
TITLE Use of locally applied dna fragments
JOURNAL Patent: WO 0174342-A 1 11-OCT-2001;
TRUSTEES OF BOSTON UNIVERSITY (US)
FEATURES
source Location/Qualifiers
1..9
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Synthetic DNA Fragment"
BASE COUNT 3 a 0 c 4 g 2 t
ORIGIN

Query Match 100.0%; Score 5; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.2e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAc 5
Db 7 CATAc 3

RESULT 9
S50583/c
LOCUS S50583 9 bp mRNA linear PRI 07-MAY-1993
DEFINITION type I procollagen [human, mRNA Mutant, 9 nt].
ACCESSION S50583
VERSION S50583.1 GI:233928
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
REFERENCE
AUTHORS Tsuneyoshi,T., Westerhausen,A., Constantinou,C.D. and Prockop,D.J.
TITLE Substitutions for glycine alpha 1-637 and glycine alpha 2-694 of
type I procollagen in lethal osteogenesis imperfecta. The
conformational strain on the triple helix introduced by a glycine
substitution can be transmitted along the helix
JOURNAL J. Biol. Chem. 266 (24), 15608-15613 (1991)
MEDLINE 91340689
PUBMED 1874719
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gibbsq 50583] from the original journal article.
This sequence comes from Fig 5A.
FEATURES
source Location/Qualifiers
1..9
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 1 a 3 c 2 g 3 t
ORIGIN

Query Match 100.0%; Score 5; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.2e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAc 5
Db 9 CATAc 5

RESULT 10
S50585/c
LOCUS S50585 9 bp DNA linear PRI 07-MAY-1993
DEFINITION type I procollagen [human, Genomic Mutant, 9 nt].
ACCESSION S50585
VERSION S50585.1 GI:233929
KEYWORDS
SOURCE Homo sapiens.

```

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 9)
Tsuneyoshi,T., Westerhausen,A., Constantinou,C.D. and Prockop,D.J.
Substitutions for glycine alpha 1-637 and glycine alpha 2-694 of
type I procollagen in lethal osteogenesis imperfecta. The
conformational strain on the triple helix introduced by a glycine
substitution can be transmitted along the helix
J. Biol. Chem. 266 (24), 15608-15613 (1991)
9340689
MEDLINE
1874719
PUBMED
GenBank staff at the National Library of Medicine created this
entry [NCBI gisbq 50585] from the original journal article.
This sequence comes from Fig 5B.
FEATURES
source
1..9
Location/Qualifiers
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/db_xref="taxon:9606"
1..9
gene
/gene="type I procollagen"
2 a 1 c 3 g 3 t
BASE COUNT
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 3.2e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CATAC 5
Db 9 CATAC 5

RESULT 11
A18263/c
LOCUS
A18263
DEFINITION oligonucleotide.
ACCESSION A18263
VERSION A18263.1 GI:512254
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
synthetic construct
artificial sequences.
1 (bases 1 to 10)
Della Valle,F., Callegaro,L. and Negro,A.
Process for the preparation of genetic vectors for the nerve growth
factor expression in eukaryotic cells
Patent: EP 0432510-A 12 19-JUN-1991;
FIDIA S.P.A.
FEATURES
source
1..10
Location/Qualifiers
/organism="synthetic construct"
/db_xref="taxon:32630"
3 a 1 c 3 g 3 t
BASE COUNT
ORIGIN

Query Match 100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CATAC 5
Db 10 CATAC 6

RESULT 12
AR065157
LOCUS
AR065157
DEFINITION Sequence 1 from patent US 5849489.
ACCESSION AR065157
VERSION AR065157.1 GI:5995373
KEYWORDS
SOURCE
Unknown.

ORGANISM Unknown.
Unclassified.
1 (bases 1 to 10)
Heller,M.J.
Hybridization of polynucleotides conjugated with chromophores and
fluorophores to generate donor-to-donor energy transfer system
Patent: US 5849489-A 1 15-DEC-1998;
JOURNAL
FEATURES
source
1..10
Location/Qualifiers
/organism="unknown"
3 a 2 c 2 g 3 t
BASE COUNT
ORIGIN

Query Match 100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CATAC 5
Db 4 CATAC 8

RESULT 13
AR079101/c
LOCUS
AR079101
DEFINITION Sequence 23 from patent US 5965409.
ACCESSION AR079101
VERSION AR079101.1 GI:10005847
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
1 (bases 1 to 10)
Pardee,A.B. and Liang,P.
System for comparing levels or amounts of mRNAs
Patent: US 5965409-A 23 12-OCT-1999;
JOURNAL
FEATURES
source
1..10
Location/Qualifiers
/organism="unknown"
1 a 1 c 3 g 4 t 1 others
BASE COUNT
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 6.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CATAC 5
Db 5 CATAC 1

RESULT 14
AR079103/c
LOCUS
AR079103
DEFINITION Sequence 25 from patent US 5965409.
ACCESSION AR079103
VERSION AR079103.1 GI:10005849
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
1 (bases 1 to 10)
Pardee,A.B. and Liang,P.
System for comparing levels or amounts of mRNAs
Patent: US 5965409-A 25 12-OCT-1999;
JOURNAL
FEATURES
source
1..10
Location/Qualifiers
/organism="unknown"
1 a 2 c 3 g 3 t 1 others
BASE COUNT
ORIGIN

Query Match 100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.8e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5
|||||
Db 5 CATAC 1

RESULT 15
AR098909/c
LOCUS AR098909 10 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 45 from patent US 6077685.
ACCESSION AR098909
VERSION AR098909.1 GI:12808675
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Trofatter,J.A., MacCollin,M.M. and Gusella,J.F.
TITLE Tumor suppressor merlin and antibodies thereof
JOURNAL Patent: US 6077685-A 45 20-JUN-2000;
FEATURES
 source
 1..10
 /organism="unknown"
BASE COUNT 2 a 2 c 3 g 3 t
ORIGIN

Query Match 100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. NO. 6.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5
|||||
Db 5 CATAC 1

Search completed: July 6, 2003, 08:29:48
Job time : 239.5 secs

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OM nucleic - nucleic search, using sw model

Run on: July 6, 2003, 06:40:37 ; Search time 110.714 Seconds
(without alignments)
101.703 Million cell updates

Title: US-09-540-843-6

Perfect score: 5

Sequence: 1 catac 5

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 2063506

Minimum DB seq length: 0

Maximum DB seq length: 40.

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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23:	/SID\$2/cgdata/geneseq/geneseqn-emb1/NA20001B.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query			ID	Description
		Match	Length	DB		
C 1	5	100.0	5	20	AAZ10695	Oligonucleotide se
C 2	5	100.0	5	20	AAZ10696	Oligonucleotide se
C 3	5	100.0	5	23	AAZ14908	Melanogenesis asso
C 4	5	100.0	5	23	AAZ14910	Melanogenesis asso
C 5	5	100.0	7	20	AAZ10694	Oligonucleotide se
C 6	5	100.0	7	23	AAZ14907	Melanogenesis asso
C 7	5	100.0	7	23	AAZ14911	Melanogenesis asso
C 8	5	100.0	8	22	AAD02250	Direct repeat sequ
C 9	5	100.0	9	19	AAV22350	A promoter regulat

ALIGNMENTS

RESULT 7

AAZ10695/C

ID AAZ10695 standard: DNA: 5 BP.

AAZ10695:

23-NOV-1999 (first entry)

XX $\text{O}(\log n) + \text{O}(n^2)$

XX

UV-induced humoral immune response; UV-induced dermatitis; UV mimetic; UV-irradiation; UV-induced dermatitis; p53 activity; UV mimetic; UV-irradiation; UV-induced dermatitis; KW

KW UV-induced hyperproliferative disease; psoriasis; vitiligo;
KW atonic dermatitis; allergic rhinitis; conductive otitis; phototoxic;

KW atopic dermatitis
KW skin cancer: se

XX
C
+
+
+
C

XX
DN CB33361E7-3

XX

XX

XX

XX

XX

XX
1551-1552

XX DNA fragments useful for increasing p53 activity in a cell and reducing

PT susceptibility to UV-induced hyperproliferative diseases -
 PS Claim 11; Page 30; 4pp; English.
 XX
 CC AZA10692-97 represent DNA fragments that are used for increasing p53
 CC activity in a cell. The oligonucleotides are UV mimetics and
 CC protect cells against subsequent exposure to UV-irradiation or
 CC chemicals. The oligonucleotides are useful for increasing p53 activity
 CC in a cell, reducing the susceptibility to UV-induced hyperproliferative
 CC diseases, treating psoriasis, vitiligo, atopic dermatitis, allergic
 CC rhinitis, conjunctivitis, and UV-induced dermatoses, reducing photoaging
 CC and reducing susceptibility to skin cancer.
 XX
 SQ Sequence 5 BP; 1 A; 0 C; 2 G; 2 T; 0 other;

Query Match 100.0%; Score 5; DB 20; Length 5;
 Best Local Similarity 100.0%; Pred. No. 4.3e+08;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAC 5
 Db 1 CATAC 1
 11111

RESULT 2
 AAZ10696 ID PN AAZ10696 standard; DNA; 5 BP.
 AC AAZ10696;
 XX
 DT 23-NOV-1999 (first entry)
 XX
 DE Oligonucleotide sequence that increases p53 activity in a cell.
 XX
 KW p53 activity; UV mimetic; UV-irradiation; UV-induced dermatosis;
 KW UV-induced hyperproliferative disease; psoriasis; vitiligo;
 KW atopic dermatitis; allergic rhinitis; conjunctivitis; photoaging;
 KW skin cancer; ss.
 XX
 OS Synthetic.
 XX
 PN GB2336157-A.
 XX
 PD 13-OCT-1999.
 XX
 PF 24-MAR-1999; 99GB-0006758.
 XX
 PR 26-MAR-1998; 98US-0048927.
 XX
 PA (UYBO-) UNIV BOSTON.
 XX
 PI Gilchrist BA, Yaar M, Eller M;
 XX
 DR WPI; 1999-543520/46.
 XX
 XX DNA fragments useful for increasing p53 activity in a cell and reducing
 PT susceptibility to UV-induced hyperproliferative diseases -
 PT
 XX Claim 11; Page 30; 4pp; English.
 XX
 CC AZA10692-97 represent DNA fragments that are used for increasing p53
 CC activity in a cell. The oligonucleotides are UV mimetics and
 CC protect cells against subsequent exposure to UV-irradiation or
 CC chemicals. The oligonucleotides are useful for increasing p53 activity
 CC in a cell, reducing the susceptibility to UV-induced hyperproliferative
 CC diseases, treating psoriasis, vitiligo, atopic dermatitis, allergic
 CC rhinitis, conjunctivitis, and UV-induced dermatoses, reducing photoaging
 CC and reducing susceptibility to skin cancer.
 XX
 SQ Sequence 5 BP; 2 A; 2 C; 0 G; 1 T; 0 other;

Query Match 100.0%; Score 5; DB 20; Length 5;
 Best Local Similarity 100.0%; Pred. No. 4.3e+08;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAC 5
 Db 1 CATAC 5
 11111

RESULT 3
 AAS14908/C
 ID AAS14908 standard; DNA; 5 BP.
 XX
 AC AAS14908;
 XX
 DT 14-FEB-2002 (first entry)
 XX
 DE Melanogenesis associated oligonucleotide #4.
 XX
 KW Melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53;
 KW anti-inflammatory; dermatological; ophthalmological; anti-psoriatic;
 KW immunosuppressive; DNA repair; proliferation inhibitor; apoptosis;
 KW tumour necrosis factor inhibitor; photoaging; hyperproliferative disease;
 KW carcinoma; oxidative stress; skin cancer; allergy mediated inflammation;
 KW conjunctivitis; allergic rhinitis; vitiligo; ss.
 XX
 OS Synthetic.
 XX
 PN WO200174342-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US10162.
 XX
 PR 31-MAR-2000; 2000US-0540843.
 XX
 PA (UYBO-) UNIV BOSTON.
 XX
 PI Gilchrist BA, Yaar M, Eller M;
 XX
 DR WPI; 2001-626338/72.
 XX
 XX Inhibiting proliferation of epithelial cells, useful e.g. for treating
 PT carcinoma, using specific oligonucleotides that mimic the effects of
 PT ultra-violet light -
 XX
 PS Claim 1; Page 36; 74pp; English.
 XX
 CC The invention describes inhibition of mammalian epithelial cell
 CC proliferation by treating cells with at least one oligonucleotide, or
 CC its fragment. The compounds, which have cytostatic, anti-allergic,
 CC anti-inflammatory, dermatological, ophthalmological, anti-psoriatic and
 CC immunosuppressive activities, function as 'ultra-violet mimics' to induce
 CC DNA repair processes (or a protective response to later exposure to
 CC radiation or chemicals), as a proliferation inhibitor, apoptosis inducer
 CC or a tumour necrosis factor inhibitor. Probably they mimic products of
 CC DNA damage, or processed DNA-damage intermediates, by inducing the p53
 CC pathway, resulting in transient arrest of cell growth, allowing more time
 CC for DNA repair to occur before cell division takes place. The method is
 CC especially used to treat carcinoma but may also be used to treat other
 CC hyperproliferative states (e.g. psoriasis or precancerous conditions);
 CC reduce photoaging, oxidative stress or damage; prevent skin cancer; treat
 CC allergically mediated inflammation (atopic or contact dermatitis,
 CC allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in
 CC cells caused by radiation or chemicals; increase melanin production
 CC (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to
 CC promote apoptosis in epithelial cells that contain damaged DNA. Also
 CC oligonucleotides that contain non-hydrolyzable backbones are used to
 CC inhibit apoptosis, in response to DNA damage, in epithelial cell. This
 CC sequence is melanogenesis associated oligonucleotide #4, a truncated
 CC version of the oligonucleotide shown in AAS14906, one of the
 CC oligonucleotides used to inhibit mammalian epithelial cell
 CC proliferation, described in the method of the invention.
 XX
 SQ Sequence 5 BP; 1 A; 0 C; 2 G; 2 T; 0 other;

Query Match 100.0%; Score 5; DB 23; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.3e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAC 5
|||||
Db 5 CATAC 1

RESULT 4

AAS14910
ID AAS14910 standard; DNA; 5 BP.

XX

AC AAS14910;

XX

DT 14-FEB-2002 (first entry)

XX

DE Melanogenesis associated oligonucleotide #6.

XX

KW Melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53;
KW anti-inflammatory; dermatological; ophthalmological; anti-psoriatic;
KW immunosuppressive; DNA repair; proliferation inhibitor; apoptosis;
KW tumour necrosis factor inhibitor; photoaging; hyperproliferative disease;
KW carcinoma; oxidative stress; skin cancer; allergy mediated inflammation;
KW conjunctivitis; allergic rhinitis; vitiligo; ss.

OS Synthetic.

XX

PN W0200174342-A2.

XX

PD 11-OCT-2001.

XX

PF 30-MAR-2001; 2001W0-US10162.

XX

PR 31-MAR-2000; 2000US-0540843.

XX

PA (UYBO-) UNIV BOSTON.

XX

PI Gilchrist BA, Yaar M, Eller M;

XX

DR WPI; 2001-626338/72.

XX

PT Inhibiting proliferation of epithelial cells, useful e.g. for treating
PT carcinoma, using specific oligonucleotides that mimic the effects of
PT ultra-violet light

XX

PS Claim 1; Page 36; 74pp; English.

XX

CC The invention describes inhibition of mammalian epithelial cell
CC proliferation by treating cells with at least one oligonucleotide, or
CC its fragment. The compounds, which have cytostatic, anti-allergic,
CC anti-inflammatory, dermatological, ophthalmological, anti-psoriatic and
CC immunosuppressive activities, function as 'ultra-violet mimics' to induce
CC DNA repair processes (or a protective response to later exposure to
CC radiation or chemicals), as a proliferation inhibitor, apoptosis inducer
CC or a tumour necrosis factor inhibitor. Probably they mimic products of
CC DNA damage, or processed DNA-damage intermediates, by inducing the p53
CC pathway, resulting in transient arrest of cell growth, allowing more time
CC for DNA repair to occur before cell division takes place. The method is
CC especially used to treat carcinoma but may also be used to: treat other
CC hyperproliferative states (e.g. psoriasis or precancerous conditions);
CC reduce photoaging, oxidative stress or damage; prevent skin cancer; treat
CC allergically mediated inflammation (atopic or contact dermatitis,
CC allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in
CC cells caused by radiation or chemicals; increase melanin production
CC (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to
CC promote apoptosis in epithelial cells that contain damaged DNA. Also
CC oligonucleotides that contain non-hydrolyzable backbones are used to
CC inhibit apoptosis, in response to DNA damage, in epithelial cell. This
CC sequence is melanogenesis associated oligonucleotide #6, one of the
CC oligonucleotides used to inhibit mammalian epithelial cell proliferation,
CC described in the method of the invention.

XX

SQ Sequence 5 BP; 2 A; 2 C; 0 G; 1 T; 0 other;

Query Match 100.0%; Score 5; DB 23; Length 5;

Best Local Similarity 100.0%; Pred. No. 4.3e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAC 5

|||||

Db 1 CATAC 5

RESULT 5

AAZ10694/c

ID AAZ10694 standard; DNA; 7 BP.

XX

AC AAZ10694;

XX

DT 23-NOV-1999 (first entry)

XX

DE Oligonucleotide sequence that increases p53 activity in a cell.

XX

KW p53 activity; UV mimetic; UV-irradiation; UV-induced dermatosis;

KW UV-induced hyperproliferative disease; psoriasis; vitiligo;

KW atopic dermatitis; allergic rhinitis; conjunctivitis; photoaging;

KW skin cancer; ss.

XX

OS Synthetic.

XX

PN GB2336157-A.

XX

PD 13-OCT-1999.

XX

PF 24-MAR-1999; 99GB-0006758.

XX

PR 26-MAR-1998; 98US-0048927.

XX

PA (UYBO-) UNIV BOSTON.

XX

PI Gilchrist BA, Yaar M, Eller M;

XX

DR WPI; 1999-543520/46.

XX

PT DNA fragments useful for increasing p53 activity in a cell and reducing
PT susceptibility to UV-induced hyperproliferative diseases -

XX

PS Claim 11; Page 30; 44pp; English.

XX

CC AAZ10692-97 represent DNA fragments that are used for increasing p53
CC activity in a cell. The oligonucleotides are used for increasing p53
CC protect cells against subsequent exposure to UV-irradiation or
CC chemicals. The oligonucleotides are useful for increasing p53 activity
CC in a cell, reducing the susceptibility to UV-induced hyperproliferative
CC diseases, treating psoriasis, vitiligo, atopic dermatitis, allergic
CC rhinitis, conjunctivitis, and UV-induced dermatoses, reducing photoaging
CC and reducing susceptibility to skin cancer.

SQ Sequence 7 BP; 3 A; 0 C; 2 G; 2 T; 0 other;

Query Match 100.0%; Score 5; DB 20; Length 7;

Best Local Similarity 100.0%; Pred. No. 3.1e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAC 5

|||||

Db 6 CATAC 2

RESULT 6

AAS14907/c

ID AAS14907 standard; DNA; 7 BP.

XX

AC AAS14907;

XX 14-FEB-2002 (first entry)
XX Melanogenesis associated oligonucleotide #3.
XX
KW Melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53;
KW anti-inflammatory; dermatological; ophthalmological; anti-psoriatic;
KW immunosuppressive; DNA repair; proliferation inhibitor; apoptosis;
KW tumour necrosis factor inhibitor; photoaging; hyperproliferative disease;
KW carcinoma; oxidative stress; skin cancer; allergy mediated inflammation;
KW conjunctivitis; allergic rhinitis; vitiligo; ss.
XX Synthetic.
XX WO200174342-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US10162.
XX
XX 31-MAR-2000; 2000US-0540843.
XX (UYBO-) UNIV BOSTON.
XX
XX Gilchrest BA, Yaar M, Eller M;
XX
XX WPI; 2001-626338/72.
XX
XX Inhibiting proliferation of epithelial cells, useful e.g. for treating
XX carcinoma, using specific oligonucleotides that mimic the effects of
XX ultra-violet light -
XX
XX Claim 1; Page 36; 74pp; English.
XX
XX The invention describes inhibition of mammalian epithelial cell
XX proliferation by treating cells with at least one oligonucleotide, or
XX its fragment. The compounds, which have cytostatic, anti-allergic,
XX anti-inflammatory, dermatological, ophthalmological, anti-psoriatic and
XX immunosuppressive activities, function as 'ultra-violet mimics' to induce
XX DNA repair processes (or a protective response to later exposure to
XX radiation or chemicals), as a proliferation inhibitor, apoptosis inducer
XX or a tumour necrosis factor inhibitor. Probably they mimic products of
XX DNA damage, or processed DNA-damage intermediates, by inducing the p53
XX pathway, resulting in transient arrest of cell growth, allowing more time
XX for DNA repair to occur before cell division takes place. The method is
XX especially used to treat carcinoma but may also be used to: treat other
XX hyperproliferative states (e.g. psoriasis or precancerous conditions);
XX reduce photoaging, oxidative stress or damage; prevent skin cancer; treat
XX allergically mediated inflammation (atopic or contact dermatitis;
XX allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in
XX cells caused by radiation or chemicals; increase melanin production
XX (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to
XX promote apoptosis in epithelial cells that contain damaged DNA. Also
XX oligonucleotides that contain non-hydrolyzable backbones are used to
XX inhibit apoptosis in epithelial cells that contain damaged DNA. This
XX sequence is melanogenesis associated oligonucleotide #3, a truncated
XX version of the oligonucleotide shown in AAS14906, one of the
XX oligonucleotides used to inhibit mammalian epithelial cell
XX proliferation, described in the method of the invention.
XX
XX Sequence 7 BP; 3 A; 0 C; 2 G; 2 T; 0 other;
XX
XX Query Match 100.0%; Score 5; DB 23; Length 7;
XX Best Local Similarity 100.0%; Pred. No. 3.1e+08;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 CATAC 5
XX
Db 6 CATAC 2
XX
XX RESULT 7
XX AAS14911/C

ID AAS14911 standard; DNA; 7 BP.
XX
AC AAS14911;
XX
DT 14-FEB-2002 (first entry)
XX
DE Melanogenesis associated oligonucleotide #7.
XX
KW Melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53;
KW anti-inflammatory; dermatological; ophthalmological; anti-psoriatic;
KW immunosuppressive; DNA repair; proliferation inhibitor; apoptosis;
KW tumour necrosis factor inhibitor; photoaging; hyperproliferative disease;
KW carcinoma; oxidative stress; skin cancer; allergy mediated inflammation;
KW conjunctivitis; allergic rhinitis; vitiligo; ss.
XX
OS Synthetic.
XX
XX
FH Key Location/Qualifiers
FT modified_base 1
FT /*tag= a
FT /mod_base= a
FT /note= "Phosphorylated"
XX
XX WO200174342-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US10162.
XX
XX 31-MAR-2000; 2000US-0540843.
XX
XX (UYBO-) UNIV BOSTON.
XX
XX Gilchrest BA, Yaar M, Eller M;
XX
XX WPI; 2001-626338/72.
XX
XX Inhibiting proliferation of epithelial cells, useful e.g. for treating
XX carcinoma, using specific oligonucleotides that mimic the effects of
XX ultra-violet light -
XX
XX Claim 1; Page 38; 74pp; English.
XX
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XX proliferation by treating cells with at least one oligonucleotide, or
XX its fragment. The compounds, which have cytostatic, anti-allergic,
XX anti-inflammatory, dermatological, ophthalmological, anti-psoriatic and
XX immunosuppressive activities, function as 'ultra-violet mimics' to induce
XX DNA repair processes (or a protective response to later exposure to
XX radiation or chemicals), as a proliferation inhibitor, apoptosis inducer
XX or a tumour necrosis factor inhibitor. Probably they mimic products of
XX DNA damage, or processed DNA-damage intermediates, by inducing the p53
XX pathway, resulting in transient arrest of cell growth, allowing more time
XX for DNA repair to occur before cell division takes place. The method is
XX especially used to treat carcinoma but may also be used to: treat other
XX hyperproliferative states (e.g. psoriasis or precancerous conditions);
XX reduce photoaging, oxidative stress or damage; prevent skin cancer; treat
XX allergically mediated inflammation (atopic or contact dermatitis;
XX allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in
XX cells caused by radiation or chemicals; increase melanin production
XX (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to
XX promote apoptosis in epithelial cells that contain damaged DNA. Also
XX oligonucleotides that contain non-hydrolyzable backbones are used to
XX inhibit apoptosis in epithelial cells that contain damaged DNA. This
XX sequence is melanogenesis associated oligonucleotide #7, one of the
XX oligonucleotides used to inhibit mammalian epithelial cell
XX proliferation, described in the method of the invention.
XX
XX Sequence 7 BP; 3 A; 0 C; 2 G; 2 T; 0 other;
XX
XX Query Match 100.0%; Score 5; DB 23; Length 7;
XX Best Local Similarity 100.0%; Pred. No. 3.1e+08;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAC 5
 Db 6 CATAC 2

Best Local Similarity 100.0%; Pred. No. 2.7e+08;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAC 5
 Db 2 CATAC 6

RESULT 8
 AAD02250
 ID AAD02250 standard; DNA; 8 BP.
 XX AAD02250;
 XX 28-MAR-2001 (first entry)
 DT
 XX Direct repeat sequence that binds to SB protein.
 DE
 XX Sleeping Beauty; SB; AdSB10; adenovirus; transposase;
 KW non-integrating viral vector; cytostatic; anti-diabetic; cardiant;
 KW neuroprotective; genetic disease; gene therapy; cancer;
 KW cystic fibrosis; diabetes; cardiovascular disease; brain malfunction;
 KW genome analysis; chemotherapy; transgenic host cell; direct repeat; ds.
 XX Unidentified.
 OS
 XX WO200068399-A2.
 PN
 XX 16-NOV-2000.
 PD
 XX 11-MAY-2000; 2000WO-US12827.
 PF
 XX 11-MAY-1999; 99US-0133569.
 PR
 XX (MINU) UNIV MINNESOTA.
 PA (SAYU) BAYLOR COLLEGE MEDICINE.
 PA (MCIV/) MCIVOR R S.
 PA (HACK/) HACKETT P B.
 PA (AGUI/) AGUILAR-CORDOVA E.
 XX
 PI Mcivor RS, Hackett PB, Aguilar-Cordova E;
 XX
 DR WPI; 2001-024870/03.
 XX
 XX Non-integrating (adenovirus-based) viral vectors useful in gene
 PT therapy, especially for treating patients suffering from a genetic
 PT disease, e.g. cystic fibrosis, diabetes, cardiovascular disease, cancer
 PT or brain malfunction -
 XX
 PS Disclosure; Page 14; 62pp; English.
 CC The patent discloses non-integrating viral vectors comprising a
 CC polynucleotide flanked by inverted repeats that bind a transposase, a
 CC transposase-encoding polynucleotide operably linked to a regulatory
 CC sequence comprising an operator, that alters expression of the
 CC transposase-encoding polynucleotide. Transposon sequences can integrate
 CC into genomic DNA whether or not the cell is dividing. AdSB10 is a SB
 CC (Sleeping Beauty) transposase-transducing adenoviral non-integrating
 CC vector. The non-integrating viral vectors are useful for treating
 CC genetic disease characterised by subnormal production of a polypeptide or
 CC RNA, e.g. for replacement of a defective gene, delivery of a polypeptide
 CC drug or supplementation of a metabolic activity. These genetic diseases
 CC include cystic fibrosis, diabetes, cardiovascular disease, cancer or
 CC brain malfunction. The non-integrating viral vectors are useful as
 CC nucleic acid delivery systems, e.g. for genome analysis or gene therapy
 CC and can also be used for applications that involve long-term production
 CC of a polypeptide. The non-integrating viral vectors are also useful for
 CC creating transgenic host cells that provide normal cells with protection
 CC against toxic side effects of chemotherapy.
 CC The sequence of the present invention is a direct repeat sequence that
 CC binds to SB protein.
 XX
 SQ Sequence 8 BP; 4 A; 3 C; 0 G; 1 T; 0 other;
 XX

Query Match 100.0%; Score 5; DB 22; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.4e+08;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAC 5
 Db 5 CATAC 1

RESULT 9
 AAV22350/c
 ID AAV22350 standard; RNA; 9 BP.
 XX AAV22350;
 AC
 XX 29-JUN-1998 (first entry)
 DT
 XX A promoter regulatory motif found in the utrons of the invention.
 DE
 XX 3' untranslated region; UTR; inhibition; gene expression; ICAM-7;
 KW interferon-gamma; IFN-gamma; major histocompatibility complex; MHC;
 KW antigen expression; gene promoter; utron; B7-1; B7-2; Fc gamma R;
 KW HIV gene expression; transplant rejection; treatment;
 KW autoimmune disease; inflammatory disease; ss.
 XX
 OS Unidentified.
 OS
 XX WO9744450-A1.
 PN
 XX 27-NOV-1997.
 PD
 XX 21-MAY-1997; 97WO-US09459.
 PF
 XX 21-MAY-1996; 96US-0646789.
 PR
 XX (UYUA) UNIV YALE.
 PA
 XX Peyman JA;
 PI
 XX WPI; 1998-018505/02.
 DR
 XX Utrons, RNA molecules containing promoter regulatory motifs -
 PT useful to suppress express expression from promoter of interest,
 PT specifically TSU nucleic acid suppression of MHC Class I and II gene
 PT expression
 XX
 PS Claim 20; Page 20; 200pp; English.
 CC The present sequence represents a promoter regulatory element,
 CC found in the utrons of the invention. Utrons are from, or are
 CC homologous to, the 3' untranslated region (UTR), of an mRNA that
 CC stimulates or inhibits a cellular response by sequence specific
 CC interactions. The utron is able to suppress constitutive and
 CC interferon-gamma (IFN-gamma) induced major histocompatibility complex
 CC (MHC) class I and class II antigen expression and expression of other
 CC antigens, the gene promoters of which contain related sequence motifs
 CC that are stimulated by the same factors which stimulate MHC class I and
 CC class II antigen expression. Such utrons can be used to regulate
 CC gene expression in a subject, e.g. a human or a cell in vitro.
 CC Specifically inhibiting MHC Class I or II, ICAM-7, B7-1, B7-2,
 CC Fc gamma R, IL-2 or HIV gene expression. They can be used to inhibit
 CC transplant rejection, or treat an autoimmune or inflammatory disease or
 CC disorder.
 XX
 SQ Sequence 9 BP; 3 A; 0 C; 3 G; 3 U; 0 other;
 XX

Query Match 100.0%; Score 5; DB 19; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.4e+08;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAC 5
 Db 5 CATAC 1

```
RESULT 10
AAV22283/c
ID AAV22283 standard; DNA; 9 BP.
XX
XX
AC AAV22283
XX
XX
DT 26-MAY-1998 (first entry)
XX
XX
DE Cyclin D transcription factor DMP1 nonamer consensus sequence.
XX
XX
KW cyclin D transcription factor; binding affinity; D-type cyclin; probe;
KW cell cycle inhibitor; tumour; detection; cancer; DMP1; competitor;
KW nonamer consensus sequence; ss.
XX
XX
OS Mus musculus.
OS Homo sapiens.
PN WO9743415-A1.
XX
XX
PD 20-NOV-1997.
XX
XX
PF 16-MAY-1997; 97WO-US08480.
XX
XX
PR 15-MAY-1997; 97US-0017815.
PR 16-MAY-1996; 96US-0017815.
PR 16-MAY-1996; 96US-0648837.
XX
XX
PA (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.
XX
XX
PI Hirai H, Inoue K, Sherr CJ;
XX
XX
DR WPI; 1998-008884/01.
XX
XX
PT Cyclin D transcription factor and related DNA - can be used to
PT develop products for treatment of, e.g. cancer
XX
XX
PS Claim 3; Page 99; 120pp; English.
XX
XX
CC This is a nonamer consensus sequence of a cyclin D transcription factor
CC DMP1. DMP1 is an amino acid polymer which has binding affinity for a
CC D-type cyclin, in vitro, and for a specific DNA nucleotide sequence and
CC is a transcription factor involved in the activation of genes that
CC prevent cell proliferation. The DMP1 nucleic acid is operatively linked
CC to an expression control sequence in an expression vector. The expression
CC vector has a transcription control sequence comprising this nonamer
CC sequence operably associated with a recombinant gene or a cassette
CC insertion site for a recombinant gene. The vector is homologously
CC recombined in a chromosome of a transgenic animal. A probe or a
CC competitor in DMP1 transactivation assays is designed based on this
CC nonamer sequence. The presence of activity of DMP1 can be determined by
CC detecting binding of DMP1 and a probe by contacting a biological sample
CC from a mammal with the probe under conditions that allow binding of the
CC probe to DMP1, where the probe contains the core sequence GTA, and where
CC the presence or activity of DMP1 is suspected in the sample. DMP1 can
CC function as a cell cycle inhibitor when expressed in a tumour cell.
CC Modulating the expression of DMP1 can be used to treat tumours and other
CC cancers. DMP1 can also be used for controlling expression of heterologous
CC proteins. Antisense sequences and ribozymes can be used to inhibit
CC expression of the transcription factor. Detecting the level and activity
CC of DMP1 in cells is useful for detection of cancer cells or
CC dysproliferative cells.
XX
XX
SQ Sequence 9 BP; 1 A; 3 C; 2 G; 3 T; 0 other;
Query Match 100.0%; Score 5; DB 19; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.4e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CATAC 5
Db 8 CATAC 4
RESULT 12
AAZ10692/c
ID AAV15899 standard; DNA; 9 BP.
XX
XX
AC AAV15899;
XX
XX
DT 26-MAY-1998 (first entry)
XX
XX
DE Cyclin D transcription factor DMP1 nonamer consensus sequence.
XX
XX
KW cyclin D transcription factor; binding affinity; D-type cyclin; probe;
KW cell cycle inhibitor; tumour; detection; cancer; DMP1; competitor;
KW nonamer consensus sequence; ss.
XX
XX
OS Mus musculus.
OS Homo sapiens.
PN WO9743415-A1.
XX
XX
PD 20-NOV-1997.
XX
XX
PF 16-MAY-1997; 97WO-US08480.
XX
XX
PR 15-MAY-1997; 97US-0017815.
PR 16-MAY-1996; 96US-0017815.
PR 16-MAY-1996; 96US-0648837.
XX
XX
PA (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.
XX
XX
PI Hirai H, Inoue K, Sherr CJ;
XX
XX
DR WPI; 1998-008884/01.
XX
XX
PT Cyclin D transcription factor and related DNA - can be used to
PT develop products for treatment of, e.g. cancer
XX
XX
PS Claim 3; Page 99; 120pp; English.
XX
XX
CC This is a nonamer consensus sequence of a cyclin D transcription factor
CC DMP1. DMP1 is an amino acid polymer which has binding affinity for a
CC D-type cyclin, in vitro, and for a specific DNA nucleotide sequence and
CC is a transcription factor involved in the activation of genes that
CC prevent cell proliferation. The DMP1 nucleic acid is operatively linked
CC to an expression control sequence in an expression vector. The expression
CC vector has a transcription control sequence comprising this nonamer
CC sequence operably associated with a recombinant gene or a cassette
CC insertion site for a recombinant gene. The vector is homologously
CC recombined in a chromosome of a transgenic animal. A probe or a
CC competitor in DMP1 transactivation assays is designed based on this
CC nonamer sequence. The presence of activity of DMP1 can be determined by
CC detecting binding of DMP1 and a probe by contacting a biological sample
CC from a mammal with the probe under conditions that allow binding of the
CC probe to DMP1, where the probe contains the core sequence GTA, and where
CC the presence or activity of DMP1 is suspected in the sample. DMP1 can
CC function as a cell cycle inhibitor when expressed in a tumour cell.
CC Modulating the expression of DMP1 can be used to treat tumours and other
CC cancers. DMP1 can also be used for controlling expression of heterologous
CC proteins. Antisense sequences and ribozymes can be used to inhibit
CC expression of the transcription factor. Detecting the level and activity
CC of DMP1 in cells is useful for detection of cancer cells or
CC dysproliferative cells.
XX
XX
SQ Sequence 9 BP; 1 A; 3 C; 2 G; 3 T; 0 other;
Query Match 100.0%; Score 5; DB 19; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.4e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CATAC 5
Db 8 CATAC 4
RESULT 11
AAV15899/c
ID AAV22283 standard; DNA; 9 BP.
XX
XX
AC AAV22283
XX
XX
DT 26-MAY-1998 (first entry)
XX
XX
DE Cyclin D transcription factor DMP1 nonamer consensus sequence.
XX
XX
KW cyclin D transcription factor; binding affinity; D-type cyclin; probe;
KW cell cycle inhibitor; tumour; detection; cancer; DMP1; competitor;
KW nonamer consensus sequence; ss.
XX
XX
OS Mus musculus.
OS Homo sapiens.
PN WO9743415-A1.
XX
XX
PD 20-NOV-1997.
XX
XX
PF 16-MAY-1997; 97WO-US08480.
XX
XX
PR 15-MAY-1997; 97US-0017815.
PR 16-MAY-1996; 96US-0017815.
PR 16-MAY-1996; 96US-0648837.
XX
XX
PA (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.
XX
XX
PI Hirai H, Inoue K, Sherr CJ;
XX
XX
DR WPI; 1998-008884/01.
XX
XX
PT Cyclin D transcription factor and related DNA - can be used to
PT develop products for treatment of, e.g. cancer
XX
XX
PS Claim 3; Page 99; 120pp; English.
XX
XX
CC This is a nonamer consensus sequence of a cyclin D transcription factor
CC DMP1. DMP1 is an amino acid polymer which has binding affinity for a
CC D-type cyclin, in vitro, and for a specific DNA nucleotide sequence and
CC is a transcription factor involved in the activation of genes that
CC prevent cell proliferation. The DMP1 nucleic acid is operatively linked
CC to an expression control sequence in an expression vector. The expression
CC vector has a transcription control sequence comprising this nonamer
CC sequence operably associated with a recombinant gene or a cassette
CC insertion site for a recombinant gene. The vector is homologously
CC recombined in a chromosome of a transgenic animal. A probe or a
CC competitor in DMP1 transactivation assays is designed based on this
CC nonamer sequence. The presence of activity of DMP1 can be determined by
CC detecting binding of DMP1 and a probe by contacting a biological sample
CC from a mammal with the probe under conditions that allow binding of the
CC probe to DMP1, where the probe contains the core sequence GTA, and where
CC the presence or activity of DMP1 is suspected in the sample. DMP1 can
CC function as a cell cycle inhibitor when expressed in a tumour cell.
CC Modulating the expression of DMP1 can be used to treat tumours and other
CC cancers. DMP1 can also be used for controlling expression of heterologous
CC proteins. Antisense sequences and ribozymes can be used to inhibit
CC expression of the transcription factor. Detecting the level and activity
CC of DMP1 in cells is useful for detection of cancer cells or
CC dysproliferative cells.
XX
XX
SQ Sequence 9 BP; 1 A; 3 C; 2 G; 3 T; 0 other;
Query Match 100.0%; Score 5; DB 19; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.4e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CATAC 5
Db 5 CATAC 1
RESULT 11
AAV15899/c
ID AAV22283 standard; DNA; 9 BP.
XX
XX
AC AAV22283
XX
XX
DT 26-MAY-1998 (first entry)
XX
XX
DE Cyclin D transcription factor DMP1 nonamer consensus sequence.
XX
XX
KW cyclin D transcription factor; binding affinity; D-type cyclin; probe;
KW cell cycle inhibitor; tumour; detection; cancer; DMP1; competitor;
KW nonamer consensus sequence; ss.
XX
XX
OS Mus musculus.
OS Homo sapiens.
PN WO9743415-A1.
XX
XX
PD 20-NOV-1997.
XX
XX
PF 16-MAY-1997; 97WO-US08480.
XX
XX
PR 15-MAY-1997; 97US-0017815.
PR 16-MAY-1996; 96US-0017815.
PR 16-MAY-1996; 96US-0646789.
XX
XX
PA (UYVA ) UNIV YALE.
XX
XX
PI Peyman JA;
XX
XX
DR WPI; 1998-018505/02.
XX
XX
PT Utrons, RNA molecules containing promoter regulatory motifs -
PT useful to suppress express expression from promoter of interest,
PT specifically TSU nucleic acid suppression of MHC Class I and II gene
PT expression
XX
XX
PS Claim 22; Page 90; 200pp; English.
XX
XX
CC The present sequence represents a GAS complement gene promoter motif
CC found in a trophoblast STAR utron (TSU). TSUs be isolated from a CDNA
CC library prepared from mRNA isolated from trophoblast cells. Utrons are
CC from, or are homologous to, the 3' untranslated region (UTR), of an mRNA
CC that stimulates or inhibits a cellular response by sequence specific
CC interactions. The TSU is able to suppress constitutive and
CC interferon-gamma (IFN-gamma) induced major histocompatibility complex
CC (MHC) class I and class II antigen expression and expression of other
CC antigens, the gene promoters of which contain related sequence motifs
CC that are stimulated by the same factors which stimulate MHC class I and
CC class II antigen expression. The TSU sequence contains motifs related to
CC IFN signalling (GAS, ISRE and interleukin-4 response elements). The
CC nucleic acid can be used to regulate gene expression in a subject, e.g. a
CC human or a cell in vitro, specifically inhibiting MHC Class I or II,
CC ICAM-7, B7-1, B7-2, Fc gamma R, IL-2 or HIV gene expression. It can be
CC used to inhibit transplant rejection, or treat an autoimmune or
CC inflammatory disease or disorder. It can also be used to inhibit the
CC action of STAT1-6, or a cytokine.
XX
XX
SQ Sequence 9 BP; 3 A; 0 C; 3 G; 3 T; 0 other;
Query Match 100.0%; Score 5; DB 19; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.4e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CATAC 5
Db 5 CATAC 1
RESULT 11
AAV15899/c
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```

ID  AAZ10692 standard; DNA; 9 BP.
XX
AC  AAZ10692;
XX
DT  23-NOV-1999 (first entry)
XX
DE  Oligonucleotide sequence that increases p53 activity in a cell.
XX
XX  p53 activity; UV mimetic; UV-irradiation; UV-induced dermatosis;
KW  UV-induced hyperproliferative disease; psoriasis; vitiligo;
KW  atopic dermatitis; allergic rhinitis; conjunctivitis; photoaging;
KW  skin cancer; ss.
XX
OS  Synthetic.
XX
XX  GB2336157-A.
PN
XX  13-OCT-1999.
PD
XX  24-MAR-1999; 99GB-0006758.
PF
XX  26-MAR-1998; 98US-0048927.
PR
XX  (UYBO-) UNIV BOSTON.
PA
XX  Gilchrest BA, Yaar M, Eller M;
PI
XX  WPI; 1999-543520/46.
DR
XX  DNA fragments useful for increasing p53 activity in a cell and reducing
XX  susceptibility to UV-induced hyperproliferative diseases -
XX
XX  Claim 11; Page 29; 44pp; English.
XX
XX  AAZ10692-97 represent DNA fragments that are used for increasing p53
XX  activity in a cell. The oligonucleotides are UV mimetics and
XX  protect cells against subsequent exposure to UV-irradiation or
XX  chemicals. The oligonucleotides are useful for increasing p53 activity
XX  in a cell, reducing the susceptibility to UV-induced hyperproliferative
XX  diseases, treating psoriasis, vitiligo, atopic dermatitis, allergic
XX  rhinitis, conjunctivitis, and UV-induced dermatoses, reducing photoaging
XX  and reducing susceptibility to skin cancer.
XX
SQ  Sequence 9 BP; 3 A; 0 C; 4 G; 2 T; 0 other;

Query Match      100.0%; Score 5; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.4e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 CATAC 5
Db  7 CATAC 3

RESULT 13
AAZ14905/c
ID  AAZ14905 standard; DNA; 9 BP.
XX
AC  AAZ14905;
XX
XX  14-FEB-2002 (first entry)
DT
XX
XX  Melanogenesis associated oligonucleotide #1.
DE
XX  Melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53;
KW  anti-inflammatory; dermatological; ophthalmological; anti-psoriatic;
KW  immunosuppressive; DNA repair; proliferation inhibitor; apoptosis;
KW  tumour necrosis factor inhibitor; photoaging; hyperproliferative disease;
KW  carcinoma; oxidative stress; skin cancer; allergy mediated inflammation;
KW  conjunctivitis; allergic rhinitis; vitiligo; ss.
XX
XX  Synthetic.
OS
XX

```

```

FH  Key modified_base 1 Location/Qualifiers
FT  /tag= a
FT  /mod_base= g
FT  /note= "Optionally phosphorylated"
XX
XX  WO200174342-A2.
PN
XX  11-OCT-2001.
PD
XX  30-MAR-2001; 2001WO-US10162.
PF
XX  31-MAR-2000; 2000US-0540843.
PR
XX  (UYBO-) UNIV BOSTON.
PA
XX  Gilchrest BA, Yaar M, Eller M;
PI
XX  WPI; 2001-626338/72.
DR
XX  Inhibiting proliferation of epithelial cells, useful e.g. for treating
XX  carcinoma, using specific oligonucleotides that mimic the effects of
XX  ultra-violet light
XX
XX  Claim 1; Page 36; 74pp; English.
XX
XX  The invention describes inhibition of mammalian epithelial cell
XX  proliferation by treating cells with at least one oligonucleotide, or
XX  its fragment. The compounds, which have cytostatic, anti-allergic,
XX  anti-inflammatory, dermatological, ophthalmological, anti-psoriatic and
XX  immunosuppressive activities, function as 'ultra-violet mimics' to induce
XX  DNA repair processes (or a protective response to later exposure to
XX  radiation or chemicals), as a proliferation inhibitor, apoptosis inducer
XX  or a tumour necrosis factor inhibitor. Probably they mimic products of
XX  DNA damage, or processed DNA-damage intermediates, by inducing the p53
XX  pathway, resulting in transient arrest of cell growth, allowing more time
XX  for DNA repair to occur before cell division takes place. The method is
XX  especially used to treat carcinoma but may also be used to treat other
XX  hyperproliferative states (e.g. psoriasis or precancerous conditions);
XX  reduce photoaging, oxidative stress or damage; prevent skin cancer; treat
XX  allergically mediated inflammation (atopic or contact dermatitis,
XX  allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in
XX  cells caused by radiation or chemicals; increase melanin production
XX  (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to
XX  promote apoptosis in epithelial cells that contain damaged DNA. Also
XX  oligonucleotides that contain non-hydrolyzable backbones are used to
XX  inhibit apoptosis, in response to DNA damage, in epithelial cell. This
XX  sequence is melanogenesis associated oligonucleotide #1, one of the
XX  oligonucleotides used to inhibit mammalian epithelial cell
XX  proliferation, described in the method of the invention.
XX
SQ  Sequence 9 BP; 3 A; 0 C; 4 G; 2 T; 0 other;

Query Match      100.0%; Score 5; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.4e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 CATAC 5
Db  7 CATAC 3

RESULT 14
ABQ71504
ID  ABQ71504 standard; DNA; 9 BP.
XX
XX  ABQ71504;
AC
XX  28-AUG-2002 (first entry)
DT
XX  Zinc finger protein related oligonucleotide target SEQ ID NO:623.
DE
XX  Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.
KW

```

XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO200242459-A2.
XX PD 30-MAY-2002.
XX PF 20-NOV-2001; 2001WO-US43438.
XX PR 20-NOV-2000; 2000US-0716637.
XX PA (SANG-) SANGAMO BIOSCIENCES INC.
XX PI Liu Q;
XX DR WPI; 2002-500284/53.
XX PT New zinc finger protein that binds to target site, useful in studying
PT gene function and for human therapeutics and plant engineering,
PT comprises first, second and third zinc fingers, ordered from N- to
PT C-terminus
XX PS Example 1; Page 45; 81pp; English.
XX CC The present invention describes a zinc finger protein (I) that binds to
CC a target site, comprising a first (F1), a second (F2), and a third (F3)
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC and a third (S3) target subsite. Also described are: (1) a polypeptide
CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC (3) designing (M) (I) involves selecting the F1 zinc finger such that
CC it binds to the S1 target subsite, selecting the F2 zinc finger such that
CC that it binds to the S2 target subsite, and selecting the F3 zinc
CC finger such that it binds to the S3 target subsite, thus designing (I)
CC that binds to a target site. (I) is useful for recognition of triplet
CC target subsites having the nucleotide G in the 5'-most position of the
CC subsite. (I) is useful in studying gene function, and for human
CC therapeutics and plant engineering. (I), (II) or (III) is useful in
CC therapeutic methods to modulate the expression of a target region within
CC a subject, in diagnostic methods for sequence specific detection of
CC target nucleic acid in a sample, and in assays to determine the
CC phenotype and function of gene expression. (I) has improved affinity
CC and specificity for their target sequences, as well as enhanced
CC biological activity. ABQ71213 to ABQ72214 and ABP48191 to ABP51230
CC represent DNA target sequences and zinc finger peptides which are given
CC in the exemplification of the present invention.
XX SQ Sequence 9 BP; 2 A; 2 C; 3 G; 2 T; 0 Other;

Query Match 100.0%; Score 5; DB 24; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.4e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAC 5
Db 2 CATAC 6

RESULT 15
ID ABQ71922/c
AB ABQ71922 standard; DNA; 9 BP.
XX AC ABQ71922;
XX 28-AUG-2002 (first entry)
XX DT Zinc finger protein related oligonucleotide target SEQ ID NO:2220.
XX DE Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.
XX KW Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.
XX OS Homo sapiens.
XX OS Synthetic.

XX WO200242459-A2.
XX PN 30-MAY-2002.
XX PD 20-NOV-2001; 2001WO-US43438.
XX PF 20-NOV-2000; 2000US-0716637.
XX PR (SANG-) SANGAMO BIOSCIENCES INC.
XX PA Liu Q;
XX PI WPI; 2002-500284/53.
XX DR New zinc finger protein that binds to target site, useful in studying
XX PT gene function and for human therapeutics and plant engineering,
XX PT comprises first, second and third zinc fingers, ordered from N- to
XX PT C-terminus
XX PS Example 1; Page 58; 81pp; English.
XX CC The present invention describes a zinc finger protein (I) that binds to
CC a target site, comprising a first (F1), a second (F2), and a third (F3)
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC and a third (S3) target subsite. Also described are: (1) a polypeptide
CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC (3) designing (M) (I) involves selecting the F1 zinc finger such that
CC it binds to the S1 target subsite, selecting the F2 zinc finger such that
CC that it binds to the S2 target subsite, and selecting the F3 zinc
CC finger such that it binds to the S3 target subsite, thus designing (I)
CC that binds to a target site. (I) is useful for recognition of triplet
CC target subsites having the nucleotide G in the 5'-most position of the
CC subsite. (I) is useful in studying gene function, and for human
CC therapeutics and plant engineering. (I), (II) or (III) is useful in
CC therapeutic methods to modulate the expression of a target region within
CC a subject, in diagnostic methods for sequence specific detection of
CC target nucleic acid in a sample, and in assays to determine the
CC phenotype and function of gene expression. (I) has improved affinity
CC and specificity for their target sequences, as well as enhanced
CC biological activity. ABQ71213 to ABQ72214 and ABP48191 to ABP51230
CC represent DNA target sequences and zinc finger peptides which are given
CC in the exemplification of the present invention.
XX SQ Sequence 9 BP; 2 A; 0 C; 4 G; 3 T; 0 Other;

Query Match 100.0%; Score 5; DB 24; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.4e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAC 5
Db 8 CATAC 4

Search completed: July 6, 2003, 08:07:21
Job time : 112.964 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 6, 2003, 06:40:37 ; Search time 132.857 Seconds
(without alignments)
101.703 Million cell updates/sec

Title: US-09-540-843-11

Perfect score: 6

Sequence: 1 ttaggg 6

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 2063506

Minimum DB seq length: 0

Maximum DB seq length: 40

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_101002.*

1: /SID22/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.*
2: /SID22/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*
3: /SID22/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.*
4: /SID22/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.*
5: /SID22/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.*
6: /SID22/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.*
7: /SID22/gcgdata/geneseq/geneseq-emb1/NA1986.DAT.*
8: /SID22/gcgdata/geneseq/geneseq-emb1/NA1987.DAT.*
9: /SID22/gcgdata/geneseq/geneseq-emb1/NA1988.DAT.*
10: /SID22/gcgdata/geneseq/geneseq-emb1/NA1989.DAT.*
11: /SID22/gcgdata/geneseq/geneseq-emb1/NA1990.DAT.*
12: /SID22/gcgdata/geneseq/geneseq-emb1/NA1991.DAT.*
13: /SID22/gcgdata/geneseq/geneseq-emb1/NA1992.DAT.*
14: /SID22/gcgdata/geneseq/geneseq-emb1/NA1993.DAT.*
15: /SID22/gcgdata/geneseq/geneseq-emb1/NA1994.DAT.*
16: /SID22/gcgdata/geneseq/geneseq-emb1/NA1995.DAT.*
17: /SID22/gcgdata/geneseq/geneseq-emb1/NA1996.DAT.*
18: /SID22/gcgdata/geneseq/geneseq-emb1/NA1997.DAT.*
19: /SID22/gcgdata/geneseq/geneseq-emb1/NA1998.DAT.*
20: /SID22/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.*
21: /SID22/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*
22: /SID22/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
23: /SID22/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SID22/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	6	100.0	6	AA05734	Telomerase oligonu
2	6	100.0	6	AA05734	Telomeric repeat s
3	6	100.0	6	AA05734	Melanogenesis asso
4	6	100.0	6	AA05734	Melanogenesis asso
5	6	100.0	6	AA05734	Bovine embryonic g
6	6	100.0	7	AA05734	Telomere of Arabid
7	6	100.0	7	AA05734	Variant of Arabid
8	6	100.0	8	AA05734	Peptide nucleic ac
9	6	100.0	8	AA05734	Peptide nucleic ac

c	10	6	100.0	8	21	AAA37558	PNA sequence #15 u
	11	6	100.0	8	21	AAA37572	PNA sequence #30 u
	12	6	100.0	8	23	AA05734	PNA 28 inhibiting
	13	6	100.0	8	23	AA05734	PNA 34 inhibiting
	14	6	100.0	9	16	AA05735	Telomerase oligonu
	15	6	100.0	9	18	AA05735	Peptide nucleic ac
	16	6	100.0	9	18	AA05735	Telomerase substra
	17	6	100.0	9	20	AA05735	Telomere motif mim
	18	6	100.0	9	21	AA05735	PNA sequence #16 u
	19	6	100.0	9	21	AA05735	Primer for human t
	20	6	100.0	9	22	AA05735	Human breast cance
	21	6	100.0	9	22	AA05735	PNA 29 inhibiting
c	22	6	100.0	9	24	AA05735	Drosophila Bicoid
	23	6	100.0	10	18	AA05735	N3 to P5 oligonuc
	24	6	100.0	10	18	AA05735	N3 to P5 oligonuc
	25	6	100.0	10	18	AA05735	Peptide nucleic ac
	26	6	100.0	10	18	AA05735	DNA oligonucleotid
c	27	6	100.0	10	18	AA05735	Peptide nucleic ac
	28	6	100.0	10	19	AA05735	Antisense oligonuc
c	29	6	100.0	10	20	AA05735	Lung cancer indica
	30	6	100.0	10	20	AA05735	Random amplified p
	31	6	100.0	10	20	AA05735	Telomere motif mim
	32	6	100.0	10	20	AA05735	Telomere motif mim
	33	6	100.0	10	21	AA05735	Human macrophage g
	34	6	100.0	10	21	AA05735	PNA sequence #7 us
c	35	6	100.0	10	21	AA05735	Template region of
	36	6	100.0	10	21	AA05735	PNA sequence #17 u
	37	6	100.0	10	21	AA05735	PNA sequence #21 u
c	38	6	100.0	10	21	AA05735	PNA sequence #29 u
	39	6	100.0	10	21	AA05735	Human dendritic ce
	40	6	100.0	10	21	AA05735	Human dendritic ce
	41	6	100.0	10	21	AA05735	Human dendritic ce
	42	6	100.0	10	21	AA05735	Human dendritic ce
	43	6	100.0	10	21	AA05735	Human dendritic ce
c	44	6	100.0	10	21	AA05735	Metastatic breast
c	45	6	100.0	10	21	AA05735	Metastatic breast

ALIGNMENTS

RESULT 1
AA05734

ID AA05734 standard; DNA; 6 BP.

XX AA05734;

AC AA05734;

DT 01-FEB-1996 (first entry)

XX Telomerase oligonucleotide substrate #1.

DE Telomerase; proliferation; telomere; hybrid; immortalised cell; anaemia;
KW transplanted; cell therapy; treatment; AIDS; leukaemia; lymphoma; ss.

XX Synthetic.

OS WO9513383-A1.

PN 18-MAY-1995.

PD 18-MAY-1995.

XX 10-NOV-1994; 94WO-US13130.

XX 12-NOV-1993; 93US-0153051.

XX 12-NOV-1993; 93US-0151477.

XX (GERO-) GERON CORP.

XX (TEXA) UNIV TEXAS SYSTEM.

XX Shay J, West MD, Wright WE;

XX WPI; 1995-224051/29.

XX Increasing telomere length in cells - to increase proliferative

PT capacity and therefore delay cellular senescence, useful in cell
 XX therapy and transplantation
 PS Claim 12; Page 29; 38pp; English.
 XX

CC Oligonucleotides AAT05734-7 are examples of telomerase substrates used
 CC to increase the proliferative capacity of normal cells that express
 CC telomerase activity. The oligonucleotides allow an increase in
 CC length of telomeres in normal cells and in hybrids of normal and
 CC immortalised cells. The increase in telomere length extends the
 CC capacity of cells to replicate, esp. those treated ex vivo and used
 CC for transplantation techniques e.g. cell therapy, for the treatment
 CC of AIDS, anaemia, leukaemia or lymphoma.
 XX

SQ Sequence 6 BP; 1 A; 0 C; 3 G; 2 T; 0 other;
 Query Match 100.0%; Score 6; DB 16; Length 6;
 Best Local Similarity 100.0%; Pred. No. 3.6e+08;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTAGGG 6
 Db 1 TTAGGG 6

RESULT 2
 ID AAX80998 standard; DNA; 6 BP.
 XX
 AC AAX80998;
 XX
 DT 13-SEP-1999 (first entry)
 XX
 DE Telomeric repeat sequence.
 XX
 KW Telomerase reverse transcriptase; TERT; mouse; telomere length assay;
 KW immunogen; enzyme; telomerase-mediated DNA replication; human; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9927113-A1.
 XX
 PD 03-JUN-1999.
 XX
 PF 25-NOV-1998; 98WO-US25211.
 XX
 PR 16-MAR-1998; 98US-0042460.
 XX
 PR 26-NOV-1997; 97US-0979742.
 XX

PA (GERO-) GERON CORP.
 XX
 PI (YESH) UNIV YESHIVA EINSTEIN COLLEGE.
 XX
 PI Allsopp R, Depinho R, Greenberg R, Morin GB;
 XX
 DR WPI; 1999-347722/29.
 XX

PT Mouse telomerase reverse transcriptase (mTERT) enzyme proteins and
 PT nucleic acids
 XX
 PS Disclosure; Page 62; 135pp; English.
 XX

CC The invention relates to a mouse telomerase reverse transcriptase (mTERT)
 CC enzyme. Compositions containing mTERT can be used in telomere length
 CC assays. Isolated mTERT is useful as an immunogen for the production of
 CC monoclonal or polyclonal antibodies. The method is useful for assessing
 CC the degree of purification and identification of new mTERT species, such
 CC as an mTERT allele, homolog or isoform, or to screen for modulators
 CC (antagonists and agonists) of telomerase-mediated DNA replication.
 CC Antagonists and agonists of mTERT can be used to modify the activity of
 CC other telomerase enzymes such as human TERT (hTERT).
 XX
 SQ Sequence 6 BP; 1 A; 0 C; 3 G; 2 T; 0 other;

Query Match 100.0%; Score 6; DB 20; Length 6;
 Best Local Similarity 100.0%; Pred. No. 3.6e+08;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6
 Db 1 TTAGGG 6

RESULT 3
 ID AAS14915 standard; DNA; 6 BP.
 XX
 AC AAS14915;
 XX
 DT 14-FEB-2002 (first entry)
 XX
 DE Melanogenesis associated oligonucleotide #11.
 XX
 KW Melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53;
 KW anti-inflammatory; dermatological; ophthalmological; anti-psoriatic;
 KW immunosuppressive; DNA repair; proliferation inhibitor; apoptosis;
 KW tumour necrosis factor inhibitor; photoaging; hyperproliferative disease;
 KW carcinoma; oxidative stress; skin cancer; allergy mediated inflammation;
 KW conjunctivitis; allergic rhinitis; vitiligo; ss.
 XX
 OS Synthetic.
 XX
 PN WO200174342-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US10162.
 XX
 PR 31-MAR-2000; 2000US-0540843.
 XX
 PA (UYBO-) UNIV BOSTON.
 XX
 PI Gilchrist BA, Yaar M, Eller M;
 XX
 DR WPI; 2001-626338/72.
 XX

PT Inhibiting proliferation of epithelial cells, useful e.g. for treating
 PT carcinoma, using specific oligonucleotides that mimic the effects of
 PT ultra-violet light
 XX
 PS Claim 1; Page 37; 74pp; English.
 XX

CC The invention describes inhibition of mammalian epithelial cell
 CC proliferation by treating cells with at least one oligonucleotide, or
 CC its fragment. The compounds, which have cytostatic, anti-allergic,
 CC anti-inflammatory, dermatological, ophthalmological, anti-psoriatic and
 CC immunosuppressive activities, function as 'ultra-violet mimics' to induce
 CC DNA repair processes (or a protective response to later exposure to
 CC radiation or chemicals), as a proliferation inhibitor, apoptosis inducer
 CC or a tumour necrosis factor inhibitor. Probably they mimic products of
 CC DNA damage, or processed DNA-damage intermediates, by inducing the p53
 CC pathway, resulting in transient arrest of cell growth, allowing more time
 CC for DNA repair to occur before cell division takes place. The method is
 CC especially used to treat carcinoma but may also be used to: treat other
 CC hyperproliferative states (e.g. psoriasis or precancerous conditions);
 CC reduce photoaging, oxidative stress or damage; prevent skin cancer; treat
 CC allergically mediated inflammation (atopic or contact dermatitis,
 CC allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in
 CC cells caused by radiation or chemicals; increase melanin production
 CC (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to
 CC promote apoptosis in epithelial cells that contain damaged DNA. Also
 CC oligonucleotides that contain non-hydrolyzable backbones are used to
 CC inhibit apoptosis, in response to DNA damage, in epithelial cell. This
 CC sequence is melanogenesis associated oligonucleotide #11, a truncated
 CC version of the sequence representing the telomere overhang sequence
 CC (AAS14909) and one of the oligonucleotides used to inhibit mammalian
 CC epithelial cell proliferation, described in the method of the invention.

XX
SQ Sequence 6 BP; 1 A; 0 C; 3 G; 2 T; 0 other;
Query Match 100.0%; Score 6; DB 23; Length 6;
Best Local Similarity 100.0%; Pred. No. 3.6e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTAGGG 6
Db 1 TTAGGG 6
RESULT 4
AAS14916/C
ID AAS14916 standard; DNA; 6 BP.
XX
AC AAS14916;
DT 14-FEB-2002 (first entry)
XX
DE Melanogenesis associated oligonucleotide #12.
XX
KW Melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53;
KW anti-inflammatory; dermatological; ophthalmological; anti-psoriatic;
KW immunosuppressive; DNA repair; proliferation inhibitor; apoptosis;
KW tumour necrosis factor inhibitor; photoaging; hyperproliferative disease;
KW carcinoma; oxidative stress; skin cancer; allergy mediated inflammation;
KW conjunctivitis; allergic rhinitis; vitiligo; ss.
XX
OS Synthetic.
XX
XX WO200174342-A2.
PN
XX
PD 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US10162.
PF
XX
PR 31-MAR-2000; 2000US-0540843.
XX
XX (UYBO-) UNIV BOSTON.
PA
XX
XX Gilchrist BA, Yaar M, Eller M;
PI
XX
XX WPI; 2001-626338/72.
DR
XX
XX Inhibiting proliferation of epithelial cells, useful e.g. for treating
PT carcinoma, using specific oligonucleotides that mimic the effects of
PT ultra-violet light
TX
XX
PS Claim 1; Page 37; 74pp; English.
XX
XX The invention describes inhibition of mammalian epithelial cell
CC proliferation by treating cells with at least one oligonucleotide, or
CC its fragment. The compounds, which have cytostatic, anti-allergic,
CC anti-inflammatory, dermatological, ophthalmological, anti-psoriatic and
CC immunosuppressive activities, function as 'ultra-violet mimics' to induce
CC DNA repair processes (or a protective response to later exposure to
CC radiation or chemicals), as a proliferation inhibitor, apoptosis inducer
CC or a tumour necrosis factor inhibitor. Probably they mimic products of
CC DNA damage, or processed DNA-damage intermediates, by inducing the p53
CC pathway, resulting in transient arrest of cell growth, allowing more time
CC for DNA repair to occur before cell division takes place. The method is
CC especially used to treat carcinoma but may also be used to: treat other
CC hyperproliferative states (e.g. psoriasis or precancerous conditions);
CC reduce photoaging, oxidative stress or damage; prevent skin cancer; treat
CC allergically mediated inflammation (atopic or contact dermatitis,
CC allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in
CC cells caused by radiation or chemicals; increase melanin production
CC (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to
CC promote apoptosis in epithelial cells that contain damaged DNA. Also
CC oligonucleotides that contain non-hydrolyzable backbones are used to
CC inhibit apoptosis, in response to DNA damage, in epithelial cell. This
CC sequence is melanogenesis associated oligonucleotide #12, the reverse

CC complementary sequence of AAS149015, a truncated version of the sequence
CC representing the telomere over-hang sequence (AAS14909), described in the
CC method of the invention.
XX
SQ Sequence 6 BP; 2 A; 3 C; 0 G; 1 T; 0 other;
Query Match 100.0%; Score 6; DB 23; Length 6;
Best Local Similarity 100.0%; Pred. No. 3.6e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTAGGG 6
Db 6 TTAGGG 1
RESULT 5
ABN73654
ID ABN73654 standard; cDNA; 6 BP.
XX
AC ABN73654;
XX
DT 03-JUL-2002 (first entry)
XX
DE Bovine embryonic germ (EG) cell cDNA EST 990913a CONFIG 1.
XX
KW Bovine; Bos taurus; EST; expressed sequence tag; totipotency;
KW development; gene; ss.
XX
OS Bos taurus.
XX
XX WO200194550-A2.
PN
XX
PD 13-DEC-2001.
XX
XX 07-JUN-2001; 2001WO-US18576.
PF
XX
PR 07-JUN-2000; 2000US-209874P.
PR
XX 06-JUN-2001; 2001US-0876143.
XX
XX (INFI-) INFIGEN INC.
XX
XX Eilertsen KJ, Pfister-Genskow M, Childs L;
PI
XX
XX WPI; 2002-351289/38.
DR
XX
XX An expressed sequence tag (EST), the expression of which, or its
PT complementary sequence, in a cell identifies the cell as a
PT developmentally competent or incompetent cell -
XX
XX Example 16; Page 210; 584pp; English.
PS
XX
XX The present invention describes an expressed sequence tag (EST), where
CC the EST is an isolated, enriched, or purified nucleic acid sequence
CC representing all or part of a gene, the expression of which, or its
CC complementary sequence, in a cell identifies the cell as a
CC developmentally competent or incompetent cell. Molecules which induce
CC developmental competence in a cell line are useful for inducing
CC totipotency in one or more cells. Molecules which induce developmental
CC incompetence in a cell line are useful for preventing a full term
CC pregnancy in an animal and inhibiting totipotency. The molecules are
CC also useful for treating a disease in an animal by inducing development
CC of one or more cells of the animal into a specific cell type. The
CC present sequence represents a bovine EST which is given in the
CC exemplification of the present invention.
XX
SQ Sequence 6 BP; 1 A; 0 C; 3 G; 2 T; 0 other;
Query Match 100.0%; Score 6; DB 24; Length 6;
Best Local Similarity 100.0%; Pred. No. 3.6e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTAGGG 6
Db 1 TTAGGG 6

```
Db      1 TTAGGG 6
RESULT 6
AAN91439/c
ID      AAN91439 standard; DNA; 7 BP.
XX
AC      AAN91439;
XX
DT      22-FEB-1990 (first entry)
XX
DE      Telomere of Arabidopsis thaliana.
XX
KW      Telomere; Arabidopsis thaliana; vector; artificial chromosomes;
KW      tandem repeat.
XX
OS      Arabidopsis thaliana.
XX
PN      WO8909219-A.
XX
PD      05-OCT-1989.
XX
PF      27-FEB-1989; 89WO-US00795.
XX
PR      24-MAR-1988; 88US-0172467.
XX
PA      (GEHO-) THE GENERAL HOSPITAL CORP.
XX
PI      Richards E, Ausubel FM;
XX
DR      WPI; 1989-309497/42.
XX
PS      Claim 28; page 50; 65pp; English.
XX
CC      Tandem repeats (1-1000) of the telomere are used in a vector for
CC      expressing specific genes in plants. They provide 'artificial
CC      chromosomes' which are maintained in the nucleus, so are not subjected to
CC      variable expression due to integration-position effects. They allow the
CC      integration of very foreign DNA without host range limitations.
CC      The telomere opt. contains variant repeats of CTTAAA. The telomere is
CC      pref. the pAtT4 plasmid (ATCC 67577).
XX
SQ      Sequence 7 BP; 3 A; 3 C; 0 G; 1 T; 0 other;
Query Match 100.0%; Score 6; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 3.1e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 TTAGGG 6
Db      6 TTAGGG 1
RESULT 7
AAN91442/c
ID      AAN91442 standard; DNA; 7 BP.
XX
AC      AAN91442;
XX
DT      22-FEB-1990 (first entry)
XX
DE      Variant of Arabidopsis thaliana telomere.
XX
KW      Variant telomere; Arabidopsis thaliana; vector; artificial chromosomes;
KW      tandem repeat.
XX
OS      Arabidopsis thaliana.
XX
PN      WO8909219-A.
XX
PD      05-OCT-1989.
XX
PF      27-FEB-1989; 89WO-US00795.
XX
PR      24-MAR-1988; 88US-0172467.
XX
PA      (GEHO-) THE GENERAL HOSPITAL CORP.
XX
PI      Richards E, Ausubel FM;
XX
DR      WPI; 1989-309497/42.
XX
PS      Claim 28; page 50; 65pp; English.
XX
CC      Tandem repeats (1-1000) of the telomere are used in a vector for
CC      expressing specific genes in plants. They provide 'artificial
CC      chromosomes' which are maintained in the nucleus, so are not subjected to
CC      variable expression due to integration-position effects. They allow the
CC      integration of very foreign DNA without host range limitations.
CC      The telomere opt. contains variant repeats of CTTAAA. The telomere is
CC      pref. the pAtT4 plasmid (ATCC 67577).
XX
SQ      Sequence 7 BP; 3 A; 3 C; 0 G; 1 T; 0 other;
Query Match 100.0%; Score 6; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 3.1e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 TTAGGG 6
Db      6 TTAGGG 1
RESULT 8
AAQ97993
ID      AAQ97993 standard; DNA; 8 BP.
XX
AC      AAQ97993;
XX
DT      19-OCT-1995 (first entry)
XX
DE      Peptide nucleic acid oligomer targeting HIV gene.
XX
KW      Peptide nucleic acid; PNA; HIV; human immunodeficiency virus;
KW      AIDS; antiviral; antisense; triple helix; ss.
XX
OS      Synthetic.
XX
FH      Key Location/Qualifiers
FT      misc_feature 1..8
FT      /tag= a
FT      /note= "at least one (and preferably all) of
FT      the backbone subunits are composed of N-acetyl
FT      N-(2-aminoethyl)glycine peptide residues, the
FT      nucleobase being attached covalently to the
FT      acetyl group and the peptide linkage being
FT      formed by condensation of the glycine
FT      carboxy group of one residue with the amino
FT      group of the 2-aminoethyl moiety in the next
FT      residue"
XX
PN      WO9504068-A.
XX
PD      09-FEB-1995.
XX
PF      28-JUL-1994; 94WO-US08517.
XX
PR      29-JUL-1993; 93US-0099718.
XX
PA      (ISIS-) ISIS PHARM INC.
XX
PI      Ecker DJ;
XX
DR      WPI; 1995-082179/11.
```

```
XX
PD      05-OCT-1989.
XX
PF      27-FEB-1989; 89WO-US00795.
XX
PR      24-MAR-1988; 88US-0172467.
XX
PA      (GEHO-) THE GENERAL HOSPITAL CORP.
XX
PI      Richards E, Ausubel FM;
XX
DR      WPI; 1989-309497/42.
XX
PS      New recombinant DNA contg. eukaryotic telomere esp. from higher plant
PS      - useful as vector for specific genes and maintained in nucleus as
PS      independent replicating molecule.
XX
CC      Claim 35; page 50; 65pp; English.
XX
CC      The DNA is a variant of the telomere of the pAtT4 plasmid (ATCC 67577).
XX
SQ      Sequence 7 BP; 3 A; 3 C; 0 G; 1 T; 0 other;
Query Match 100.0%; Score 6; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 3.1e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 TTAGGG 6
Db      6 TTAGGG 1
RESULT 8
AAQ97993
ID      AAQ97993 standard; DNA; 8 BP.
XX
AC      AAQ97993;
XX
DT      19-OCT-1995 (first entry)
XX
DE      Peptide nucleic acid oligomer targeting HIV gene.
XX
KW      Peptide nucleic acid; PNA; HIV; human immunodeficiency virus;
KW      AIDS; antiviral; antisense; triple helix; ss.
XX
OS      Synthetic.
XX
FH      Key Location/Qualifiers
FT      misc_feature 1..8
FT      /tag= a
FT      /note= "at least one (and preferably all) of
FT      the backbone subunits are composed of N-acetyl
FT      N-(2-aminoethyl)glycine peptide residues, the
FT      nucleobase being attached covalently to the
FT      acetyl group and the peptide linkage being
FT      formed by condensation of the glycine
FT      carboxy group of one residue with the amino
FT      group of the 2-aminoethyl moiety in the next
FT      residue"
XX
PN      WO9504068-A.
XX
PD      09-FEB-1995.
XX
PF      28-JUL-1994; 94WO-US08517.
XX
PR      29-JUL-1993; 93US-0099718.
XX
PA      (ISIS-) ISIS PHARM INC.
XX
PI      Ecker DJ;
XX
DR      WPI; 1995-082179/11.
```

XX Oligomer hybridisable to HIV sequence and contg. peptide nucleic
PT acid sub-unit - binds in complementary manner to DNA and RNA, and
PT useful for modulating HIV viral activity, e.g. in treating AIDS
XX
PS Claim 2; Page 176; 186pp; English.
XX
CC New peptide nucleic acid (PNA) oligomers are provided which (a) consist
CC of naturally occurring nucleobases covalently bound to a polyamide
CC backbone and (b) hybridise to the translation initiation AUG region,
CC 5' untranslated region (5' UTR), 3' untranslated region (3' UTR),
CC splice junctions or coding sequence of a human immunodeficiency virus
CC gene chosen from env, gag, pol, rev and tat.
CC The PNAs can be used to target RNA and single stranded DNA (ssDNA) to
CC produce antisense-type gene regulation moieties. They have utility
CC as gene-targeted drugs for modulating HIV processes. Hence they
CC can be used to treat AIDS and other viral infections. They are also
CC useful in diagnostic applications and as research tools.
CC PNA oligomers have high affinity for complementary single stranded DNA.
CC They are also able to form triple helices in which a first PNA strand
CC binds with RNA or ssDNA and a second PNA strand binds with the resulting
CC double helix or with the first PNA strand. The PNAs possess no
CC significant charge and are water soluble, which facilitates cellular
CC uptake. Further, since they contain amides of non-biological amino acids,
CC they are biostable and resistant to enzymatic degradation by proteases.
CC The present sequence is a specifically claimed PNA sequence
CC (represented by the sequence of nucleobases) targeting HIV genes.
XX
SQ Sequence 8 BP; 1 A; 0 C; 3 G; 4 T; 0 other;

Query Match 100.0%; Score 6; DB 16; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.7e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6
|||||
Db 1 TTAGGG 6

RESULT 9
AAT89239
ID AAT89239 standard; DNA; 8 BP.
XX
AC AAT89239;
XX
DT 12-MAY-1998 (first entry)
XX
DE Peptide nucleic acid 14, targeted to mammalian telomerase.
XX
KW Peptide nucleic acid; PNA; cancer; telomerase; probe; hybridisation;
KW inhibitor; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..8
FT /*tag= a
FT /note= "Sugar-phosphate backbone has been replaced by
FT a peptide backbone"
XX
PN W09738013-A1.
XX
XX 16-OCT-1997.
XX
XX 09-APR-1997; 97WO-US05931.
XX
XX 09-APR-1996; 96US-0630019.
XX
XX (GERO-) GERON CORP.
XX
XX Corey D, Norton JC, Piatyszek MA, Shay JW, Wright WE;
XX
XX WPI; 1997-512647/47.

XX New peptide nucleic acids hybridising to mammalian telomerase RNA -
PT used to inhibit telomerase for treating tumours and other
PT proliferative diseases, also for diagnosis
XX
PS Claim 9; Page 59; 76pp; English.
XX
CC This sequence is a novel peptide nucleic acid (PNA), which acts as
CC an inhibitor of mammalian, preferably human, telomerase. The PNAs
CC hybridise specifically to an RNA component of mammalian telomerase,
CC and include the sequence GGG for specific hybridisation to the template
CC region of this component. PNAs can be used as probes to detect the
CC RNA component of mammalian telomerase and as inhibitors of telomerase
CC activity, especially in the treatment of cancer.
XX
SQ Sequence 8 BP; 1 A; 0 C; 4 G; 3 T; 0 other;

Query Match 100.0%; Score 6; DB 18; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.7e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6
|||||
Db 2 TTAGGG 7

RESULT 10
AAA37558
ID AAA37558 standard; DNA; 8 BP.
XX
AC AAA37558;
XX
DT 15-AUG-2000 (first entry)
XX
DE PNA sequence #15 used to inhibit telomerase activity.
XX
KW Peptide nucleic acid; PNA; telomerase; ribonucleoprotein enzyme; cancer;
KW inhibitor; neoplasia; neurodegenerative disease; aging; hyperplasia;
KW AIDS; HIV; fungal infection; forensic identification; detect; tumour;
KW paternity testing; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 1..8
FT /*tag= a
FT /note= "Peptide nucleic acid molecule, where
FT N-(2-aminoethyl)glycine units are linked to
FT nucleotide bases via glycine amino N through a
FT methylenecarbonyl linker"
XX
PN US6046307-A.
XX
XX 04-APR-2000.
XX
XX 09-APR-1997; 97US-0838545.
XX
XX 09-APR-1996; 96US-0630019.
XX
XX (TEXA) UNIV TEXAS SYSTEM.
XX
XX Wright WE, Piatyszek MA, Shay JW, Norton JC, Corey DR;
XX
XX WPI; 2000-292432/25.
XX
XX New peptide nucleic acid (PNA) compounds that inhibit telomerase
PT activity in mammalian cells is useful as probes to detect the RNA
PT component of a mammalian telomerase -
XX
XX Claim 6; Column 71; 45pp; English.
XX
XX The present sequence represents a peptide nucleic acid molecule which
CC hybridises to the mRNA component of mammalian telomerase, and inhibits

CC telomerase activity. Telomerase is a ribonucleoprotein enzyme that
 CC synthesizes one strand of the telomeric DNA, using as a template an 11
 CC nucleotide sequence contained within the RNA component of the enzyme. The
 CC invention relates to PNA molecules having a sequence of no more than 25
 CC bases, which include the sequence GTTAGG. The uncharged nature of the PNA
 CC backbone increases the melting temperature of associating strands,
 CC increases the rate of association with targeted nucleic acids, and
 CC affords greater resistance of degradation by proteases or nucleases. The
 CC therapeutic PNAs may be used for treating disease conditions such as
 CC cancers, neoplasia, hyperplasia, neurodegenerative diseases, aging, human
 CC immunodeficiency virus (HIV) infection/AIDS (acquired immunodeficiency
 CC syndrome) and associated pathologies, fungal infections, and other
 CC diseases characterized by abnormal telomere metabolism or telomerase
 CC activity, in combination with antineoplastic and other cytotoxic or
 CC cytostatic agents, antifungal agents, and other nucleotides. PNAs may be
 CC used for molecular diagnostics, labelled PNAs are used as hybridization
 CC probes to detect or quantitate polynucleotides having a human telomerase
 CC RNA (hTR) sequence. PNA probes are also used for forensic identification
 CC of individuals, e.g. paternity testing, based on hTR gene restriction
 CC fragment length polymorphism (RFLP) pattern. PNAs are also useful as
 CC probes to detect the RNA component of a mammalian telomerase and as
 CC inhibitors of telomerase activity. The method of the present invention
 CC allows cancerous conditions to be detected with increased confidence and
 CC possibly at an earlier stage, before cells are detected as cancerous
 CC based on pathological characteristics. The diagnostic and prognostic
 CC methods of the present invention can be used to detect an immortal or
 CC neoplastic cell or tumour tissue or cancer of any origin, provided the
 CC cell expresses telomerase activity and its RNA component.

XX
 SQ Sequence 8 BP; 1 A; 0 C; 4 G; 3 T; 0 other;

Query Match 100.0%; Score 6; DB 21; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.7e+08;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTAGGG 6
 Db 2 TTAGGG 7

RESULT 11
 AAA37572/C
 ID AAA37572 standard; DNA; 8 BP.

XX AAA37572;

XX 15-AUG-2000 (first entry)

XX PNA sequence #30 used to inhibit telomerase activity.

XX Peptide nucleic acid; PNA; telomerase; ribonucleoprotein enzyme; cancer;
 KW inhibitor; neoplasia; neurodegenerative disease; aging; hyperplasia;
 KW AIDS; HIV; fungal infection; forensic identification; detect; tumour;
 KW paternity testing; ss.

XX Synthetic.

XX Key Location/Qualifiers
 FH misc_feature 1..8

FT /*tag= a
 FT /note= "Peptide nucleic acid molecule, where
 FT N-(2-aminoethyl)glycine units are linked to
 FT nucleotide bases via glycine amino N through a
 FT methylenecarbonyl linker"

XX US6046307-A.

PN 04-APR-2000.

XX 09-APR-1997; 97US-0838545.

XX 09-APR-1996; 96US-0630019.

XX

PA (TEXA) UNIV TEXAS SYSTEM.

XX Wright WE, Piatyszek MA, Shay JW, Norton JC, Corey DR;

XX WPT; 2000-292432/25.

XX New peptide nucleic acid (PNA) compounds that inhibit telomerase
 PT activity in mammalian cells is useful as probes to detect the RNA
 PT component of a mammalian telomerase

PS Example 2; Column 33; 45pp; English.

XX The present sequence represents a peptide nucleic acid molecule which
 CC hybridises to the mRNA component of mammalian telomerase, and inhibits
 CC telomerase activity. Telomerase is a ribonucleoprotein enzyme that
 CC synthesizes one strand of the telomeric DNA, using as a template an 11
 CC nucleotide sequence contained within the RNA component of the enzyme. The
 CC invention relates to PNA molecules having a sequence of no more than 25
 CC bases, which include the sequence GTTAGG. The uncharged nature of the PNA
 CC backbone increases the melting temperature of associating strands,
 CC increases the rate of association with targeted nucleic acids, and
 CC affords greater resistance of degradation by proteases or nucleases. The
 CC therapeutic PNAs may be used for treating disease conditions such as
 CC cancers, neoplasia, hyperplasia, neurodegenerative diseases, aging, human
 CC immunodeficiency virus (HIV) infection/AIDS (acquired immunodeficiency
 CC syndrome) and associated pathologies, fungal infections, and other
 CC diseases characterized by abnormal telomere metabolism or telomerase
 CC activity, in combination with antineoplastic and other cytotoxic or
 CC cytostatic agents, antifungal agents, and other nucleotides. PNAs may be
 CC used for molecular diagnostics, labelled PNAs are used as hybridization
 CC probes to detect or quantitate polynucleotides having a human telomerase
 CC RNA (hTR) sequence. PNA probes are also used for forensic identification
 CC of individuals, e.g. paternity testing, based on hTR gene restriction
 CC fragment length polymorphism (RFLP) pattern. PNAs are also useful as
 CC probes to detect the RNA component of a mammalian telomerase and as
 CC inhibitors of telomerase activity. The method of the present invention
 CC allows cancerous conditions to be detected with increased confidence and
 CC possibly at an earlier stage, before cells are detected as cancerous
 CC based on pathological characteristics. The diagnostic and prognostic
 CC methods of the present invention can be used to detect an immortal or
 CC neoplastic cell or tumour tissue or cancer of any origin, provided the
 CC cell expresses telomerase activity and its RNA component.

XX Sequence 8 BP; 3 A; 4 C; 0 G; 1 T; 0 other;

Query Match 100.0%; Score 6; DB 21; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.7e+08;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTAGGG 6
 Db 7 TTAGGG 2

RESULT 12
 AAS15436
 ID AAS15436 standard; DNA; 8 BP.

XX AAS15436;

XX 14-FEB-2002 (first entry)

XX PNA 28 inhibiting human and mammalian telomerase activity.

XX Mammalian; peptide nucleic acid; probe; forensic; paternity testing;
 KW human telomerase RNA component; hTR gene RFLP pattern; cancer;
 KW inflammation; lymphoproliferative disease; autoimmune disease;
 KW neurodegenerative disease; neoplasia; hyperplasia; HIV; AIDS;
 KW human immunodeficiency virus; acquired immunodeficiency syndrome;
 KW telomere metabolism; mutant; cytostatic; anti-inflammatory;
 KW immunosuppressive; polyamide backbone; ss.

XX Homo sapiens.

QY 1 TTAGGG 6
 Db 2 TTAGGG 7

RESULT 14

AAT05735
 ID AAT05735 standard; DNA; 9 BP.

XX AC AAT05735;

XX DT 01-FEB-1996 (first entry)

XX DE Telomerase oligonucleotide substrate #2.

XX KW Telomerase; proliferation; telomere; hybrid; immortalised cell; anaemia;
 transplplantation; cell therapy; treatment; AIDS; leukaemia; lymphoma; ss.

XX OS Synthetic.

XX PN WO9513383-A1.

XX PD 18-MAY-1995.

XX PF 10-NOV-1994; 94WO-US13130.

XX PR 12-NOV-1993; 93US-0153051.

XX PR 12-NOV-1993; 93US-0151477.

XX PA (GERO-) GERON CORP.

XX PA (TEXA) UNIV TEXAS SYSTEM.

XX PI Shay J, West MD, Wright WE;

XX DR WPI; 1995-224051/29.

XX PT Increasing telomere length in cells - to increase proliferative
 capacity and therefore delay cellular senescence, useful in cell
 therapy and transplantation

XX PS Claim 12; Page 29; 38pp; English.

XX CC Oligonucleotides AAT05734-7 are examples of telomerase substrates used
 to increase the proliferative capacity of normal cells that express
 telomerase activity. The oligonucleotides allow an increase in
 length of telomeres in normal cells and in hybrids of normal and
 immortalised cells. The increase in telomere length extends the
 capacity of cells to replicate, esp. those treated ex vivo and used
 for transplantation techniques e.g. cell therapy, for the treatment
 of AIDS, anaemia, leukaemia or lymphoma.

XX SQ Sequence 9 BP; 2 A; 0 C; 3 G; 4 T; 0 other;

Query Match 100.0%; Score 6; DB 16; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.4e+08;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6
 Db 1 TTAGGG 6

RESULT 15

AAT89240

ID AAT89240 standard; DNA; 9 BP.

XX AC AAT89240;

XX DT 12-MAY-1998 (first entry)

XX DE Peptide nucleic acid 15, targeted to mammalian telomerase.

XX KW Peptide nucleic acid; PNA; cancer; telomerase; probe; hybridisation;

KW inhibitor; ss.

XX OS Synthetic.

XX Key Location/Qualifiers

FT modified_base 1..9

FT /*tag= a

FT /note= "Sugar-phosphate backbone has been replaced by
 a peptide backbone"

XX PN WO9738013-A1.

XX PD 16-OCT-1997.

XX PF 09-APR-1997; 97WO-US05931.

XX PR 09-APR-1996; 96US-0630019.

XX PA (GERO-) GERON CORP.

XX PI Corey D, Norton JC, Piatyszek MA, Shay JW, Wright WE;

XX DR WPI; 1997-512647/47.

XX PT New peptide nucleic acids hybridising to mammalian telomerase RNA -
 used to inhibit telomerase, for treating tumours and other
 proliferative diseases, also for diagnosis

XX PS Claim 9; Page 59; 76pp; English.

XX CC This sequence is a novel peptide nucleic acid (PNA), which acts as
 an inhibitor of mammalian, preferably human, telomerase. The PNAs
 hybridise specifically to an RNA component of mammalian telomerase,
 and include the sequence GGG for specific hybridisation to the template
 region of this component. PNAs can be used as probes to detect the
 RNA component of mammalian telomerase and as inhibitors of telomerase
 activity, especially in the treatment of cancer.

XX SQ Sequence 9 BP; 2 A; 0 C; 4 G; 3 T; 0 other;

Query Match 100.0%; Score 6; DB 18; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.4e+08;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6

Db 3 TTAGGG 8

Search completed: July 6, 2003, 08:07:24

Job time : 135.107 secs

GenCore version 5.1.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 6, 2003, 06:42:31 ; Search time 285 seconds
(without alignments)
612.691 Million cell updates/sec

Title: US-09-540-843-11

Perfect score: 6

Sequence: 1 ttaggg 6

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 774614

Minimum DB seq length: 0

Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*
2: gb_hcg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pi.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*
15: em_ba.*
16: em_fun.*
17: em_hum.*
18: em_in.*
19: em_mu.*
20: em_on.*
21: em_ov.*
22: em_sy.*
23: em_pat.*
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25: em_pi.*
26: em_ro.*
27: em_sts.*
28: em_un.*
29: em_vi.*
30: em_hcg_hum.*
31: em_hcg_inv.*
32: em_hcg_other.*
33: em_hcg_mus.*
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35: em_hcg_rod.*
36: em_hcg_mam.*
37: em_hcg_vrt.*
38: em_sy.*
39: em_higo_hum.*
40: em_higo_mus.*
41: em_higo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	6	100.0	6	6	AX055801	Sequence
C 2	6	100.0	6	6	AX058275	Sequence
C 3	6	100.0	6	6	AX175285	Sequence
C 4	6	100.0	6	6	AX268763	Sequence
C 5	6	100.0	6	6	AX268764	Sequence
C 6	6	100.0	10	6	AR026485	Sequence
C 7	6	100.0	10	6	AX152177	Sequence
C 8	6	100.0	10	6	AX153381	Sequence
C 9	6	100.0	10	6	AX153382	Sequence
C 10	6	100.0	10	6	AX153383	Sequence
C 11	6	100.0	10	6	AX153524	Sequence
C 12	6	100.0	10	6	BD011231	Human tel
C 13	6	100.0	10	6	E36980	Human telom
C 14	6	100.0	11	6	AR016034	Sequence
C 15	6	100.0	11	6	AR026486	Sequence
C 16	6	100.0	11	6	AR026487	Sequence
C 17	6	100.0	11	6	AR059195	Sequence
C 18	6	100.0	11	6	AR075506	Sequence
C 19	6	100.0	11	6	AR161904	Sequence
C 20	6	100.0	11	6	AX033373	Sequence
C 21	6	100.0	11	6	AX268757	Sequence
C 22	6	100.0	11	6	AX268761	Sequence
C 23	6	100.0	11	6	AX283296	Sequence
C 24	6	100.0	11	6	AX394462	Sequence
C 25	6	100.0	11	6	AX394499	Sequence
C 26	6	100.0	11	6	AX471710	Sequence
C 27	6	100.0	11	6	BD003369	Mammalian
C 28	6	100.0	11	6	I31749	Sequence 2
C 29	6	100.0	12	6	A21302	Nucleotide
C 30	6	100.0	12	6	AR026476	Sequence
C 31	6	100.0	12	6	AR026477	Sequence
C 32	6	100.0	12	6	AR026480	Sequence
C 33	6	100.0	12	6	AR050933	Sequence
C 34	6	100.0	12	6	AR050934	Sequence
C 35	6	100.0	12	6	AR050938	Sequence
C 36	6	100.0	12	6	AR059223	Sequence
C 37	6	100.0	12	6	AR059544	Sequence
C 38	6	100.0	12	6	AR059545	Sequence
C 39	6	100.0	12	6	AR075547	Sequence
C 40	6	100.0	12	6	AR134878	Sequence
C 41	6	100.0	12	6	AR134879	Sequence
C 42	6	100.0	12	6	AR193363	Sequence
C 43	6	100.0	12	6	AR200885	Sequence
C 44	6	100.0	12	6	AR204552	Sequence
C 45	6	100.0	12	6	AR204553	Sequence

ALIGNMENTS

RESULT 1
AX055801/c
LOCUS AX055801 6 bp DNA linear PAT 13-JAN-2001
DEFINITION Sequence 5 from Patent WO0073420.
ACCESSION AX055801
VERSION AX055801.1 GI:12228914
KEYWORDS synthetic construct,
synthetic construct,
artificial sequences.
SOURCE 1 (bases 1 to 6)
ORGANISM Hahn, W.C. and Weinberg, R.A.
REFERENCE Creation of human tumorigenic cells and uses therefor
AUTHORS Patent: WO 0073420-A 5 07-DEC-2000;
TITLE WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; DANA-FARBER
JOURNAL

FEATURES
source
CANCER INSTITUTE, INC. (US)
Location/Qualifiers
1..6
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="synthetic primer"
BASE COUNT 2 a 3 c 0 g 1 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 4.8e+09;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6
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Db 6 TTAGGG 1

RESULT 2
AX058275
LOCUS AX058275 6 bp DNA linear PAT 17-JAN-2001
DEFINITION Sequence 10 from Patent WO0074667.
ACCESSION AX058275
VERSION AX058275.1 GI:12310774
KEYWORDS synthetic construct.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Au, J.L. and Wientjes, G.
TITLE Compositions active in telomere damage comprising a taxane and telomerase inhibitor
JOURNAL Patent: WO 0074667-A 10 14-DEC-2000;
Au, Jessie L.S. (US); Wientjes, Guillaume (US)
FEATURES Location/Qualifiers
source 1..6
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="primer/probe"
BASE COUNT 1 a 0 c 3 g 2 t
ORIGIN

Query Match 100.0%; Score 6; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.8e+09;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6
|||||
Db 1 TTAGGG 6

RESULT 3
AX175285
LOCUS AX175285 6 bp DNA linear PAT 03-JUL-2001
DEFINITION Sequence 49 from Patent WO0144465.
ACCESSION AX175285
VERSION AX175285.1 GI:14598653
KEYWORDS synthetic construct.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 6)
AUTHORS Phillips, N.C. and Fillion, M.C.
TITLE Therapeutically useful synthetic oligonucleotides
JOURNAL Patent: WO 0144465-A 49 21-JUN-2001;
Bioniche Life Sciences Inc. (CA)
FEATURES Location/Qualifiers
source 1..6
/organism="synthetic construct"
/db_xref="taxon:32630"
BASE COUNT 1 a 0 c 3 g 2 t
ORIGIN

Query Match 100.0%; Score 6; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.8e+09;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6
|||||
Db 1 TTAGGG 6

RESULT 4
AX268763
LOCUS AX268763 6 bp DNA linear PAT 29-OCT-2001
DEFINITION Sequence 11 from Patent WO0174342.
ACCESSION AX268763
VERSION AX268763.1 GI:16541835
KEYWORDS synthetic construct.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Gilchrist, B.A., Yaar, M. and Eller, M.
TITLE Use of locally applied dna fragments
JOURNAL Patent: WO 0174342-A 11 11-OCT-2001;
TRUSTEES OF BOSTON UNIVERSITY (US)
FEATURES Location/Qualifiers
source 1..6
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Synthetic DNA Fragment"
BASE COUNT 1 a 0 c 3 g 2 t
ORIGIN

Query Match 100.0%; Score 6; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.8e+09;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6
|||||
Db 1 TTAGGG 6

RESULT 5
AX268764
LOCUS AX268764 6 bp DNA linear PAT 29-OCT-2001
DEFINITION Sequence 12 from Patent WO0174342.
ACCESSION AX268764
VERSION AX268764.1 GI:16541836
KEYWORDS synthetic construct.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Gilchrist, B.A., Yaar, M. and Eller, M.
TITLE Use of locally applied dna fragments
JOURNAL Patent: WO 0174342-A 12 11-OCT-2001;
TRUSTEES OF BOSTON UNIVERSITY (US)
FEATURES Location/Qualifiers
source 1..6
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Synthetic DNA Fragment"
BASE COUNT 2 a 3 c 0 g 1 t
ORIGIN

Query Match 100.0%; Score 6; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.8e+09;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6
|||||
Db 6 TTAGGG 11

RESULT 6
AR026485
LOCUS AR026485 10 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 10 from patent US 5856096.
ACCESSION AR026485
VERSION AR026485.1 GI:5937325
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Windle, B.E., Qiu, M., Chen, S.-F., Fletcher, T.M. and Maine, I.
TITLE Rapid and sensitive assays for detecting and distinguishing between
progressive and non-progressive telomerase activities
JOURNAL Patent: US 5856096-A 10 05-JAN-1999;
FEATURES
source 1..10
Location/Qualifiers
BASE COUNT 2 a 0 c 4 g 4 t
ORIGIN
Query Match 100.0%; Score 6; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.9e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTAGGG 6
Db 1 TTAGGG 6
RESULT 7
AX152177
LOCUS AX152177 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 92 from Patent WO0138577.
ACCESSION AX152177
VERSION AX152177.1 GI:14533828
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Velculescu, V.E., Vogelstein, B. and Kinzler, K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 92 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES
source 1..10
Location/Qualifiers
BASE COUNT 3 a 2 c 3 g 2 t
ORIGIN
Query Match 100.0%; Score 6; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.9e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTAGGG 6
Db 2 TTAGGG 7
RESULT 8
AX153381/c
LOCUS AX153381 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 1296 from Patent WO0138577.
ACCESSION AX153381
VERSION AX153381.1 GI:14535032
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 10)
AUTHORS Velculescu, V.E., Vogelstein, B. and Kinzler, K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 1296 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES
source 1..10
Location/Qualifiers
BASE COUNT 5 a 3 c 0 g 2 t
ORIGIN
Query Match 100.0%; Score 6; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.9e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTAGGG 6
Db 8 TTAGGG 3
RESULT 9
AX153382/c
LOCUS AX153382 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 1297 from Patent WO0138577.
ACCESSION AX153382
VERSION AX153382.1 GI:14535033
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Velculescu, V.E., Vogelstein, B. and Kinzler, K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 1297 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES
source 1..10
Location/Qualifiers
BASE COUNT 5 a 3 c 0 g 2 t
ORIGIN
Query Match 100.0%; Score 6; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.9e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTAGGG 6
Db 8 TTAGGG 3
RESULT 10
AX153383/c
LOCUS AX153383 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 1298 from Patent WO0138577.
ACCESSION AX153383
VERSION AX153383.1 GI:14535034
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Velculescu, V.E., Vogelstein, B. and Kinzler, K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 1298 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES
source 1..10
Location/Qualifiers
BASE COUNT 5 a 3 c 0 g 2 t
ORIGIN
Query Match 100.0%; Score 6; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.9e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTAGGG 6
Db 8 TTAGGG 3

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BASE COUNT      5 a      3 c      0 g      2 t
ORIGIN

Query Match      100.0%; Score 6; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.9e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6
Db      |||||
8 TTAGGG 3

RESULT 11
AXI53524
LOCUS      AXI53524
DEFINITION Sequence 1439 from Patent WO0138577.
ACCESSION AXI53524
VERSION AXI53524.1 GI:14535175
KEYWORDS
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 10)
Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
Human transcripts
Patent: WO 0138577-A 1439 31-MAY-2001;
The Johns Hopkins University (US)
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Source      1..10
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BASE COUNT      1 a      1 c      5 g      3 t
ORIGIN

Query Match      100.0%; Score 6; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.9e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6
Db      |||||
5 TTAGGG 10

RESULT 12
BD011231
LOCUS      BD011231
DEFINITION Human telomerase catalytic subunit.
ACCESSION BD011231
VERSION BD011231.1 GI:18639604
KEYWORDS JP 2001081042-A/188.
SOURCE      unidentified.
ORGANISM      unclassified.
REFERENCE      1 (bases 1 to 10)
AUTHORS      Sechi,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Mori,G.B.,
Harley,C.B. and Andrews,W.H.
TITLE      Human telomerase catalytic subunit
JOURNAL      Patent: JP 2001081042-A 188 27-MAR-2001;
GERON CORP.UNIVERSITY TECHNOLOGY CORP
COMMENT      OS Unidentified
PN JP 2001081042-A/188
PD 27-MAR-2001
PF 27-JUL-2000 JP 2000227474
PR 01-OCT-1996 US 08/724643,18-APR-1997 US 08/844419 PR
25-APR-1997 US 08/846017,06-MAY-1997 US 08/851843 PR
09-MAY-1997 US 08/854050,14-AUG-1997 US 08/911312 PR
14-AUG-1997 US 08/912951,14-AUG-1997 US 08/915503 PI THOMAS
R SECHI,JOACHIM LINGNER,TORU NAKAMURA,KAREN B CHAPMAN,PI GREG B
MORIN,
PI CALVIN B HARLEY,WILLIAM H ANDREWS
PC A61K38/00,A61K31/7088,A61K39/00,A61K48/00,A61P35/00,A61P43/00,
PC C07K5/10,

BASE COUNT      5 a      3 c      0 g      2 t
ORIGIN

Query Match      100.0%; Score 6; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.9e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6
Db      |||||
5 TTAGGG 10

RESULT 13
E36980
LOCUS      E36980
DEFINITION Human telomerase catalytic subunit promoter.
ACCESSION E36980
VERSION E36980.1 GI:13022943
KEYWORDS JP 1999253177-A/188.
SOURCE      unidentified.
ORGANISM      unclassified.
REFERENCE      1 (bases 1 to 10)
AUTHORS      Thomas,R.S., Jochimu,R., Toru,N., Karen,B.C., Greg,B.M.,
Calvin,B.H. and William,H.A.
TITLE      Human telomerase catalytic subunit promoter
JOURNAL      Patent: JP 1999253177-A 188 21-SEP-1999;
JERON CORP.UNIVERSITY TECHNOLOGY CORP
COMMENT      OS Unidentified
PN JP 1999253177-A/188
PD 21-SEP-1999
PF 15-OCT-1998 JP 1998320169
PR 01-OCT-1996 US 08/772463,18-APR-1997 US 08/844419, PR
25-APR-1997 US 08/846017,06-MAY-1997 US 08/851843, PR
09-MAY-1997 US 08/854050,14-AUG-1997 US 08/911312, PR
14-AUG-1997 US 08/912951,14-AUG-1997 US 08/915503 PI THOMAS
R SECHI,JOCHIMU RINGNER,TORU NAKAMURA,KAREN B CHAPMAN,PI GREG B
MORIN,
PI CALVIN B HARET,WILLIAM H ANDREWS
PC C12N15/09,A61K31/70,A61K38/55,A61K39/395,A61K48/00,
PC C12N1/02,
PC C12N1/48,C12Q1/68,G01N33/15,G01N33/48,G01N33/50/C07K14/47, PC
C07K16/40.
PC C12N1/19,C12N1/21,C12N5/10,C12N9/12,C12P21/08, (C12N1/19, PC
C12R1:84),
PC (C12N1/21,C12R1:19), (C12N9/12,C12R1:19), (C12N9/12,C12R1:84),
PC (C12N9/12,C12R1:91),C12N15/00,A61K37/64,C12N5/00 CC
Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
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/organism="Unidentified"
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BASE COUNT      2 a      0 c      4 g      4 t
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FEATURES
Source      1..10
Location/Qualifiers
/organism="Unidentified"
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Query Match      100.0%; Score 6; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.9e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6
Db      |||||
1 TTAGGG 6

RESULT 14
E36980
LOCUS      E36980
DEFINITION Human telomerase catalytic subunit promoter.
ACCESSION E36980
VERSION E36980.1 GI:13022943
KEYWORDS JP 1999253177-A/188.
SOURCE      unidentified.
ORGANISM      unclassified.
REFERENCE      1 (bases 1 to 10)
AUTHORS      Thomas,R.S., Jochimu,R., Toru,N., Karen,B.C., Greg,B.M.,
Calvin,B.H. and William,H.A.
TITLE      Human telomerase catalytic subunit promoter
JOURNAL      Patent: JP 1999253177-A 188 21-SEP-1999;
JERON CORP.UNIVERSITY TECHNOLOGY CORP
COMMENT      OS Unidentified
PN JP 1999253177-A/188
PD 21-SEP-1999
PF 15-OCT-1998 JP 1998320169
PR 01-OCT-1996 US 08/772463,18-APR-1997 US 08/844419, PR
25-APR-1997 US 08/846017,06-MAY-1997 US 08/851843, PR
09-MAY-1997 US 08/854050,14-AUG-1997 US 08/911312, PR
14-AUG-1997 US 08/912951,14-AUG-1997 US 08/915503 PI THOMAS
R SECHI,JOCHIMU RINGNER,TORU NAKAMURA,KAREN B CHAPMAN,PI GREG B
MORIN,
PI CALVIN B HARET,WILLIAM H ANDREWS
PC C12N15/09,A61K31/70,A61K38/55,A61K39/395,A61K48/00,
PC C12N1/02,
PC C12N1/48,C12Q1/68,G01N33/15,G01N33/48,G01N33/50/C07K14/47, PC
C07K16/40.
PC C12N1/19,C12N1/21,C12N5/10,C12N9/12,C12P21/08, (C12N1/19, PC
C12R1:84),
PC (C12N1/21,C12R1:19), (C12N9/12,C12R1:19), (C12N9/12,C12R1:84),
PC (C12N9/12,C12R1:91),C12N15/00,A61K37/64,C12N5/00 CC
Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..10
/organism="Unidentified"
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/db_xref="taxon:32644"
BASE COUNT      2 a      0 c      4 g      4 t
ORIGIN

FEATURES
Source      1..10
Location/Qualifiers
/organism="Unidentified"
/db_xref="taxon:32644"
4 t

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Query Match 100.0%; Score 6; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.9e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTAGGG 6
|||||
Db 1 TTAGGG 6

RESULT 14
AR016034/c
LOCUS AR016034 11 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 2 from patent US 5776679.
ACCESSION AR016034
VERSION AR016034.1 GI:3972311
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 11)
Villemonteu, B., Feng, J., Funk, W. and Andrews, W. H.
Assays for the DNA component of human telomerase
TITLE Assays for the DNA component of human telomerase
JOURNAL Patent: US 5776679-A 2 07-JUL-1998;
FEATURES
location/Qualifiers
source
1..11
/organism="unknown"

BASE COUNT 4 a 5 c 0 g 2 t
ORIGIN

Query Match 100.0%; Score 6; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.8e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTAGGG 6
|||||
Db 10 TTAGGG 5

RESULT 15
AR026486
LOCUS AR026486 11 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 11 from patent US 5856096.
ACCESSION AR026486
VERSION AR026486.1 GI:5937326
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 11)
Windle, B. E., Qiu, M., Chen, S.-F., Fletcher, T. M. and Maine, I.
Rapid and sensitive assays for detecting and distinguishing between
processive and non-processive telomerase activities
TITLE Rapid and sensitive assays for detecting and distinguishing between
JOURNAL Patent: US 5856096-A 11 05-JAN-1999;
FEATURES
location/Qualifiers
source
1..11
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BASE COUNT 2 a 0 c 5 g 4 t
ORIGIN

Query Match 100.0%; Score 6; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.8e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTAGGG 6
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Search completed: July 6, 2003, 08:29:51
Job time : 286 secs

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Job time : 65.5714 secs

Best Local Similarity 100.0%; Pred. No. 1.7e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0;

QY 1 TTAGGG 6
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Db 6 TTAGGG 1

RESULT 14

US-10-044-692-294
; Sequence 294, Application US/10044692
; Publication No. US20030096344A1

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.

TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
THERAPEUTIC METHODS

NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/044,692
FILING DATE: 11-Jan-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/912,951
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996

ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-00260005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 294:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA

SEQUENCE DESCRIPTION: SEQ ID NO: 294:

US-10-044-692-294

Query Match 100.0%; Score 6; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0;

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| | | | |
Db 6 TTAGGG 1

QY 1 TTAGGG 6
| | | | |
Db 1 TTAGGG 6

RESULT 15

US-10-044-539-294
; Sequence 294, Application US/10044539
; Publication No. US20030100093A1

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.

TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
THERAPEUTIC METHODS

NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/044,539
FILING DATE: 11-Jan-2002
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/912,951
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996

ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-00260005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 294:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA

SEQUENCE DESCRIPTION: SEQ ID NO: 294:

US-10-044-539-294

Query Match 100.0%; Score 6; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0;

QY 1 TTAGGG 6
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Db 1 TTAGGG 6

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Oy 1 TTAGGG 6
Db 1 TTAGGG 6

RESULT 10
US-09-730-893-6
; Sequence 6, Application US/09730893
; Patent No. US20020107258A1
; GENERAL INFORMATION:
; APPLICANT: KERWIN, SEAN M.
; APPLICANT: FEDOROFF, OLEG Y.
; APPLICANT: SALAZAR, MIGUEL
; APPLICANT: HURLEY, LAURENCE H.
; TITLE OF INVENTION: INHIBITION OF HUMAN TELOMERASE BY A
; FILE REFERENCE: G-QUADRUPLIX-INTERACTION COMPOUND
; CURRENT APPLICATION NUMBER: US/09/730,893
; CURRENT FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 09/244,675
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: 60/073,629
; PRIOR FILING DATE: 1998-04-02
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 7
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-09-730-893-6

Query Match 100.0%; Score 6; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.2e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTAGGG 6
Db 1 TTAGGG 6

RESULT 11
US-09-940-173A-4
; Sequence 4, Application US/09940173A
; Publication No. US20030040525A1
; GENERAL INFORMATION:
; APPLICANT: KERWIN, SEAN M.
; APPLICANT: FEDOROFF, OLEG Y.
; APPLICANT: SALAZAR, MIGUEL
; APPLICANT: HURLEY, LAURENCE H.
; TITLE OF INVENTION: INHIBITION OF HUMAN TELOMERASE BY A
; FILE REFERENCE: UTSB:679USD2
; CURRENT APPLICATION NUMBER: US/09/940,173A
; CURRENT FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: 09/730,893
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 09/244,675
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: 60/073,629
; PRIOR FILING DATE: 1998-04-02
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 8
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer

Oy 1 TTAGGG 6
Db 1 TTAGGG 6

RESULT 12
US-09-730-893-4
; Sequence 4, Application US/09730893
; Patent No. US20020107258A1
; GENERAL INFORMATION:
; APPLICANT: KERWIN, SEAN M.
; APPLICANT: FEDOROFF, OLEG Y.
; APPLICANT: SALAZAR, MIGUEL
; APPLICANT: HURLEY, LAURENCE H.
; TITLE OF INVENTION: INHIBITION OF HUMAN TELOMERASE BY A
; FILE REFERENCE: UTSB:679USCI
; CURRENT APPLICATION NUMBER: US/09/730,893
; CURRENT FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 09/244,675
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: 60/073,629
; PRIOR FILING DATE: 1998-04-02
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 8
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-09-730-893-4

Query Match 100.0%; Score 6; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTAGGG 6
Db 1 TTAGGG 6

RESULT 13
US-09-728-574-19/c
; Sequence 19, Application US/09728574
; Patent No. US20020137036A1
; GENERAL INFORMATION:
; APPLICANT: Stratagene
; TITLE OF INVENTION: Methods for Detection of a Target Nucleic Acid By Capture
; FILE REFERENCE: 25436/1660
; CURRENT APPLICATION NUMBER: US/09/728,574
; CURRENT FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 09/728574
; PRIOR FILING DATE: 2000-11-30
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Drosophila sp.
; NAME/KEY: bicoid DNA binding site
; LOCATION: (1)..(9)
US-09-728-574-19

Query Match 100.0%; Score 6; DB 10; Length 9;
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Best Local Similarity 100.0%; Pred. No. 2.5e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6
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Db 1 TTAGGG 6

RESULT 6

US-09-817-387-29
; Sequence 29, Application US/09817387
; Patent No. US20010039263A1
; GENERAL INFORMATION:
; APPLICANT: Max-Delbruck-Centrum fur Molekulare Medizin
; TITLE OF INVENTION: Chimeric Oligonucleotides and the Use Thereof
; FILE REFERENCE: 101195-24
; CURRENT APPLICATION NUMBER: US/09/817,387
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: DE 197 20 151.2
; PRIOR FILING DATE: 1997-05-02
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: telomeric
; OTHER INFORMATION: DNA of man

US-09-817-387-29

Query Match 100.0%; Score 6; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6
|||||
Db 1 TTAGGG 6

RESULT 7

US-09-735-363A-49
; Sequence 49, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
; APPLICANT: Phillip, Mario
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 49
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide

US-09-735-363A-49

Query Match 100.0%; Score 6; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6
|||||
Db 1 TTAGGG 6

RESULT 8

US-09-730-893-1
; Sequence 1, Application US/09730893
; Patent No. US20020107258A1
; GENERAL INFORMATION:
; APPLICANT: KERWIN, SEAN M.
; APPLICANT: FEDOROFF, OLEG Y.
; APPLICANT: SALAZAR, MIGUEL
; APPLICANT: HURLEY, LAURENCE H.
; TITLE OF INVENTION: INHIBITION OF HUMAN TELOMERASE BY A
; FILE REFERENCE: UTSB:679USD1
; CURRENT APPLICATION NUMBER: US/09/730,893
; CURRENT FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 09/244,675
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: 60/073,629
; PRIOR FILING DATE: 1998-04-02
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer

US-09-730-893-1

Query Match 100.0%; Score 6; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6
|||||
Db 1 TTAGGG 6

RESULT 9

US-09-940-173A-6
; Sequence 6, Application US/09940173A
; Publication No. US20030040525A1
; GENERAL INFORMATION:
; APPLICANT: KERWIN, SEAN M.
; APPLICANT: FEDOROFF, OLEG Y.
; APPLICANT: SALAZAR, MIGUEL
; APPLICANT: HURLEY, LAURENCE H.
; TITLE OF INVENTION: INHIBITION OF HUMAN TELOMERASE BY A
; FILE REFERENCE: UTSB:679USD2
; CURRENT APPLICATION NUMBER: US/09/940,173A
; CURRENT FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: 09/730,893
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 09/244,675
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: 60/073,629
; PRIOR FILING DATE: 1998-04-02
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 7
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer

US-09-940-173A-6

Query Match 100.0%; Score 6; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.2e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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RESULT 2
US-10-122-630-12/c
; Sequence 12, Application US/10122630
; Publication No. US20030032610A1
; GENERAL INFORMATION:
; APPLICANT: Gilchrist, Barbara A.
; APPLICANT: Eller, Mark S.
; APPLICANT: Yaar, Mina
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using
; TITLE OF INVENTION: Oligonucleotides
; FILE REFERENCE: 0054.1088-018
; CURRENT APPLICATION NUMBER: US/10/122,630
; CURRENT FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 08/467,012
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: PCT/US96/08386
; PRIOR FILING DATE: 1996-06-03
; PRIOR APPLICATION NUMBER: US 09/048,927
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: US 09/540,843
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: PCT/US01/10162
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-630-12

Query Match      100.0%; Score 6; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TTAGGG 6
Db      6 TTAGGG 1

RESULT 3
US-10-122-633-11
; Sequence 11, Application US/10122633
; Publication No. US20030032611A1
; GENERAL INFORMATION:
; APPLICANT: Gilchrist, Barbara A.
; APPLICANT: Eller, Mark S.
; APPLICANT: Yaar, Mina
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using
; TITLE OF INVENTION: Oligonucleotides
; FILE REFERENCE: 0054.1088-019
; CURRENT APPLICATION NUMBER: US/10/122,633
; CURRENT FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 09/540,843
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: PCT/US01/10162
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-633-11

Query Match      100.0%; Score 6; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TTAGGG 6
Db      6 TTAGGG 1
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RESULT 4
US-10-122-633-12/c
; Sequence 12, Application US/10122633
; Publication No. US20030032611A1
; GENERAL INFORMATION:
; APPLICANT: Gilchrist, Barbara A.
; APPLICANT: Eller, Mark S.
; APPLICANT: Yaar, Mina
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using
; TITLE OF INVENTION: Oligonucleotides
; FILE REFERENCE: 0054.1088-019
; CURRENT APPLICATION NUMBER: US/10/122,633
; CURRENT FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 09/540,843
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: PCT/US01/10162
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-633-12

Query Match      100.0%; Score 6; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TTAGGG 6
Db      6 TTAGGG 1

RESULT 5
US-09-940-173A-1
; Sequence 1, Application US/09940173A
; Publication No. US20030040525A1
; GENERAL INFORMATION:
; APPLICANT: FEDOROFF, SEAN M.
; APPLICANT: SALAZAR, MIGUEL
; APPLICANT: HURLEY, LAURENCE H.
; TITLE OF INVENTION: INHIBITION OF HUMAN TELOMERASE BY A
; TITLE OF INVENTION: G-QUADRUPLIX-INTERACTION COMPOUND
; FILE REFERENCE: UTSB:679USD2
; CURRENT APPLICATION NUMBER: US/09/940,173A
; CURRENT FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: 09/730,893
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 09/244,675
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: 60/073,629
; PRIOR FILING DATE: 1998-04-02
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-09-940-173A-1

Query Match      100.0%; Score 6; DB 9; Length 6;
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 6, 2003, 08:30:00 ; Search time 65.5714 Seconds
(without alignments)
142.836 Million cell updates/sec

Title: US-09-540-843-11

Perfect score: 6

Sequence: 1 ttaggg 6

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1085931 seqs, 780495707 residues

Total number of hits satisfying chosen parameters: 816406

Minimum DB seq length: 0

Maximum DB seq length: 40

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	6	100.0		6	9	US-10-122-630-11	Sequence 11, Appl
C 2	6	100.0		6	9	US-10-122-630-12	Sequence 12, Appl
3	6	100.0		6	9	US-10-122-633-11	Sequence 11, Appl
C 4	6	100.0		6	9	US-10-122-633-12	Sequence 12, Appl
5	6	100.0		6	9	US-09-940-173A-1	Sequence 1, Appl
6	6	100.0		6	10	US-09-817-387-29	Sequence 29, Appl
7	6	100.0		6	10	US-09-735-363A-49	Sequence 49, Appl
8	6	100.0		6	10	US-09-730-893-1	Sequence 1, Appl
9	6	100.0		7	9	US-09-940-173A-6	Sequence 6, Appl
10	6	100.0		7	10	US-09-730-893-6	Sequence 6, Appl
11	6	100.0		8	9	US-09-940-173A-4	Sequence 4, Appl
12	6	100.0		8	10	US-09-730-893-4	Sequence 4, Appl
C 13	6	100.0		9	10	US-09-728-574-19	Sequence 19, Appl
14	6	100.0		10	9	US-10-044-692-294	Sequence 294, App
15	6	100.0		10	9	US-10-044-539-294	Sequence 294, App
16	6	100.0		10	12	US-10-033-145-56	Sequence 56, Appl
17	6	100.0		10	12	US-10-033-145-358	Sequence 358, App
18	6	100.0		10	12	US-10-033-145-613	Sequence 613, App
19	6	100.0		10	12	US-10-033-145-1694	Sequence 1694, App

20	6	100.0	11	9	US-09-835-370-63	Sequence 63, Appl
21	6	100.0	11	9	US-10-122-630-5	Sequence 5, Appl
c 22	6	100.0	11	9	US-10-122-630-9	Sequence 9, Appl
23	6	100.0	11	9	US-10-122-633-5	Sequence 5, Appl
c 24	6	100.0	11	9	US-10-122-633-9	Sequence 9, Appl
c 25	6	100.0	11	9	US-09-249-155-57	Sequence 57, Appl
c 26	6	100.0	11	9	US-09-942-310-7	Sequence 7, Appl
27	6	100.0	11	9	US-09-942-310-44	Sequence 44, Appl
c 28	6	100.0	11	9	US-10-038-335-9	Sequence 9, Appl
c 29	6	100.0	11	10	US-09-057-351-2	Sequence 2, Appl
c 30	6	100.0	12	8	US-08-463-404-2	Sequence 3, Appl
31	6	100.0	12	8	US-08-463-404-3	Sequence 7, Appl
c 32	6	100.0	12	8	US-08-463-404-7	Sequence 1, Appl
c 33	6	100.0	12	8	US-10-132-002-1	Sequence 3, Appl
34	6	100.0	12	9	US-10-132-002-3	Sequence 18, Appl
c 35	6	100.0	12	9	US-10-073-118-18	Sequence 41, Appl
36	6	100.0	12	9	US-10-117-108A-41	Sequence 53, Appl
c 37	6	100.0	12	9	US-10-117-108A-53	Sequence 11, Appl
38	6	100.0	12	9	US-09-984-664-11	Sequence 39, Appl
39	6	100.0	12	10	US-09-057-351-39	Sequence 1, Appl
40	6	100.0	12	10	US-09-968-355-1	Sequence 6, Appl
41	6	100.0	12	10	US-09-375-924C-6	Sequence 4, Appl
42	6	100.0	13	9	US-09-893-252-4	Sequence 1, Appl
43	6	100.0	13	9	US-10-038-335-1	Sequence 2, Appl
44	6	100.0	13	9	US-10-038-335-2	Sequence 123, App
45	6	100.0	14	8	US-08-591-486B-123	

ALIGNMENTS

RESULT 1

US-10-122-630-11

; Sequence 11, Application US/10122630

; Publication No. US20030032610A1

; GENERAL INFORMATION:

; APPLICANT: Gilchrist, Barbara A.

; APPLICANT: Eller, Mark S.

; APPLICANT: Yaar, Mina

; TITLE OF INVENTION: Method to Inhibit Cell Growth Using

; FILE REFERENCE: 0054.1088-018

; CURRENT FILING DATE: 2002-04-12

; PRIOR FILING DATE: 2002-04-12

; PRIOR APPLICATION NUMBER: US 08/467,012

; PRIOR FILING DATE: 1995-06-06

; PRIOR APPLICATION NUMBER: PCT/US96/08386

; PRIOR FILING DATE: 1996-06-03

; PRIOR APPLICATION NUMBER: US 09/048,927

; PRIOR FILING DATE: 1998-03-26

; PRIOR APPLICATION NUMBER: US 09/540,843

; PRIOR FILING DATE: 2000-03-31

; PRIOR APPLICATION NUMBER: PCT/US01/10162

; PRIOR FILING DATE: 2001-03-30

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 11

; LENGTH: 6

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic DNA Fragment

US-10-122-630-11

Query Match 100.0%; Score 6; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTAGGG 6

Db 1 TTAGGG 6

SEQUENCE CHARACTERISTICS:
LENGTH: 7 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: DNA (genomic)
US-08-729-598-8

Query Match 100.0%; Score 6; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+07;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6
Db 2 TTAGGG 7

RESULT 15
US-08-838-545-15
Sequence 15, Application US/08838545
Patent No. 6046307
GENERAL INFORMATION:
APPLICANT: Shay, Jerry W.
APPLICANT: Wright, Woodring E.
APPLICANT: Platyszek, Mieczyslaw A.
APPLICANT: Corey, David R.
APPLICANT: No. 6046307ton, James C.
TITLE OF INVENTION: Modulation of Mammalian Telomerase by
TITLE OF INVENTION: Peptide Nucleic Acids
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,545
FILING DATE: 09-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,019
FILING DATE: 09-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-001610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "peptide nucleic acid (PNA),
DESCRIPTION: where (deoxy/ribose-phosphate linkages are replaced by
DESCRIPTION: N-(2-aminoethyl)glycine units linked to nucleotide bases via
DESCRIPTION: glycine amino N through a methylenecarbonyl linker"
US-08-838-545-15

Query Match 100.0%; Score 6; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 3.6e+07;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6
Db 2 TTAGGG 7

Search completed: July 6, 2003, 09:42:20
Job time : 31.0714 secs

TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-018-545-3

Query Match 100.0%; Score 6; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.8e+07;
Matches 6; Conservative 0; Mismatches 0; Indels 0;

QY 1 TTAGGG 6
|||||
DB 1 TTAGGG 6

RESULT 12

US-09-114-399-3
Sequence 3, Application US/09114399
Patent No. 6245747
GENERAL INFORMATION:
APPLICANT: Porter, Thomas R.
APPLICANT: Iversen, Patrick L.
APPLICANT: Meyer, Gary D.

TITLE OF INVENTION: Targeted Site Specific Drug Delivery
TITLE OF INVENTION: Compositions and Method of Use
FILE REFERENCE: 0450-0310.31
CURRENT APPLICATION NUMBER: US/09/114,399
CURRENT FILING DATE: 1998-07-13
PRIOR APPLICATION NUMBER: US 08/615,495
PRIOR FILING DATE: 1996-03-12

NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3

LENGTH: 6
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: PS-ODN
US-09-114-399-3

Query Match 100.0%; Score 6; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.8e+07;
Matches 6; Conservative 0; Mismatches 0; Indels 0;

QY 1 TTAGGG 6
|||||
DB 1 TTAGGG 6

RESULT 13

PCT-US96-01206-1
Sequence 1, Application PC/TUS9601206
GENERAL INFORMATION:

APPLICANT: Iverson, Patrick L.
APPLICANT: Mata, John E.

TITLE OF INVENTION: Synthetic Oligodeoxynucleotides Which
Mimic Telomeric Sequences for Use in the Treatment of
Cancer and other Diseases

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Zarley, McKee, Thomte, Voorhees & Sease
STREET: 801 Grand Avenue Suite 3200

CITY: Des Moines

STATE: Iowa

COUNTRY: United States

ZIP: 50309

COMPUTER READABLE FORM: disk

MEDIUM TYPE: Floppy

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/01206

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/381,097

FILING DATE: 31-JAN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Nebel, Heidi S.

REGISTRATION NUMBER: 37,719

REFERENCE/DOCKET NUMBER: UNMC# 63092

TELECOMMUNICATION INFORMATION:

TELEPHONE: 515-288-3667

TELEFAX: 515-288-1338

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 6 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

HYPOTHETICAL: NO

ANTI-SENSE: YES

PCT-US96-01206-1

Query Match 100.0%; Score 6; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.8e+07;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1 TTAGGG 6
|||||
DB 1 TTAGGG 6

RESULT 14

US-08-729-598-8
Sequence 8, Application US/08729598
Patent No. 6001657

GENERAL INFORMATION:

APPLICANT: Hardin, Charles C.

APPLICANT: Brown II, Bernard A.

APPLICANT: Roberts, John J.

APPLICANT: Pelsue, Stephen A.

TITLE OF INVENTION: Antibodies That Selectively Bind

Quadruplex Nucleic Acids

TITLE OF INVENTION: Quadruplex Nucleic Acids

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sorojini J. Biswas

STREET: P.O. Box 37428

CITY: Raleigh

STATE: No. 6001657th Carolina

COUNTRY: USA

ZIP: 27627

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/729,598

FILING DATE: 11-OCT-1996

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Biswas, Sorojini J.

REGISTRATION NUMBER: 39,111

REFERENCE/DOCKET NUMBER: 5051-301A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (919) 854-1400

TELEFAX: (919) 854-1401

INFORMATION FOR SEQ ID NO: 8:

APPLICANT: Nam Woo Kim
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
CONDITIONS RELATED TO
TITLE OF INVENTION: TELOMERE LENGTH AND/OR
TELOMERASE ACTIVITY
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,867
FILING DATE: March 14, 1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/153,051
FILING DATE: No. 6007989ember 12, 1993
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Chambers, Daniel M.
REGISTRATION NUMBER: 34,561
REFERENCE/DOCKET NUMBER: 224/232
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-819-867-27

Query Match 100.0%; Score 6; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.8e+07;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTAGGG 6
Db 6 TTAGGG 1

RESULT 10
US-08-630-019A-1
Sequence 1, Application US/08630019A
Patent No. 6015710
GENERAL INFORMATION:
APPLICANT: Shay, Jerry W.
APPLICANT: Wright, Woodring E.
APPLICANT: Platyszek, Mieczyslaw A.
APPLICANT: Corey, David
APPLICANT: No. 6015710ton, James C.
TITLE OF INVENTION: Modulation of Mammalian Telomerase by
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California

COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,019A
FILING DATE: 09-JUN-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-001600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid (PNA).
DESCRIPTION: /desc = "peptide nucleic acid (PNA).
DESCRIPTION: where (deoxy)ribose-phosphate linkages are replaced by
DESCRIPTION: N-(2-aminoethyl)glycine units linked to nucleotide bases via
DESCRIPTION: glycine amino nitrogen through a methylenecarbonyl linker"
US-08-630-019A-1

Query Match 100.0%; Score 6; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.8e+07;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTAGGG 6
Db 1 TTAGGG 6

RESULT 11
US-09-018-545-3
Sequence 3, Application US/09018545
Patent No. 6087493
GENERAL INFORMATION:
APPLICANT: Wheelhouse, Richard T.
APPLICANT: Hurley, Laurence H.
TITLE OF INVENTION: PORPHYRIN COMPOUNDS AS TELOMERASE
INHIBITORS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: U.S.
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/018,545
FILING DATE: Concurrently Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/037,295
FILING DATE: 05-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: UTSB:654

ANTI-SENSE: YES
US-08-670-999-3

Query Match 100.0%; Score 6; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.8e+07;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTAGGG 6
|||||
Db 1 TTAGGG 6

RESULT 7

US-08-729-598-4
; Sequence 4, Application US/08729598
; Patent No. 6001657
; GENERAL INFORMATION:
; APPLICANT: Hardin, Charles C.
; APPLICANT: Brown II, Bernard A.
; APPLICANT: Roberts, John J.
; APPLICANT: Pelsue, Stephen A.
; TITLE OF INVENTION: Antibodies That Selectively Bind
; TITLE OF INVENTION: Quadruplex Nucleic Acids
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sorofini J. Biswas
; STREET: P.O. Box 37428
; CITY: Raleigh
; STATE: NO. 6001657th Carolina
; COUNTRY: USA
; ZIP: 27627
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/729,598
; FILING DATE: 11-OCT-1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Biswas, Sorofini J.
; REGISTRATION NUMBER: 39,111
; REFERENCE/DOCKET NUMBER: 5051-301A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 854-1400
; TELEFAX: (919) 854-1401
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: not relevant
; MOLECULE TYPE: DNA (genomic)
US-08-729-598-4

Query Match 100.0%; Score 6; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.8e+07;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTAGGG 6
|||||
Db 1 TTAGGG 6

RESULT 8

US-08-819-867-9
; Sequence 9, Application US/08819867
; Patent No. 6007989
; GENERAL INFORMATION:
; APPLICANT: Michael D. West
; APPLICANT: Calvin B. Harley
; APPLICANT: Scott L. Weinrich

; APPLICANT: Catherine M. Strahl
; APPLICANT: Michael J. Mceachern
; APPLICANT: Jerry Shay
; APPLICANT: Woodring E. Wright
; APPLICANT: Elizabeth H. Blackburn
; APPLICANT: Nam Woo Kim
; APPLICANT: Homayoun Vaziri
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
; TITLE OF INVENTION: CONDITIONS RELATED TO
; TITLE OF INVENTION: TELOMERASE LENGTH AND/OR
; TITLE OF INVENTION: TELOMERASE ACTIVITY
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/819,867
; FILING DATE: March 14, 1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/153,051
; FILING DATE: No. 6007989ember 12, 1993
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Chambers, Daniel M.
; REGISTRATION NUMBER: 34,561
; REFERENCE/DOCKET NUMBER: 224/232
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELETYPE: 67-3510
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-819-867-9

Query Match 100.0%; Score 6; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.8e+07;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTAGGG 6
|||||
Db 1 TTAGGG 6

RESULT 9

US-08-819-867-27/c
; Sequence 27, Application US/08819867
; Patent No. 6007989
; GENERAL INFORMATION:
; APPLICANT: Michael D. West
; APPLICANT: Calvin B. Harley
; APPLICANT: Scott L. Weinrich
; APPLICANT: Catherine M. Strahl
; APPLICANT: Michael J. Mceachern
; APPLICANT: Jerry Shay
; APPLICANT: Woodring E. Wright
; APPLICANT: Elizabeth H. Blackburn

;; SOFTWARE: Word Perfect 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/337,684
;; FILING DATE: No. 5686306ember 10, 1994
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/151,477
;; FILING DATE: No. 5686306ember 12, 1993
;; APPLICATION NUMBER: 08/153,051
;; FILING DATE: No. 5686306ember 12, 1993
;; APPLICATION NUMBER: 08/060,952
;; FILING DATE: May 13, 1993
;; APPLICATION NUMBER: 08/038,766
;; FILING DATE: March 24, 1993
;; APPLICATION NUMBER: 07/882,438
;; FILING DATE: May 13, 1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Warburg, Richard J.
;; REGISTRATION NUMBER: 32,327
;; REFERENCE/DOCKET NUMBER: 210/085
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (213) 489-1600
;; TELEFAX: (213) 955-0440
;; TELEX: 67-3510
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 6 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; US-08-337-684-2

Query Match 100.0%; Score 6; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.8e+07;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6
Db 1 TTAGGG 6

RESULT 5
US-08-151-477A-4/c
;; Sequence 4, Application US/08151477A
;; Patent No. 5830644
;; GENERAL INFORMATION:
;; APPLICANT: Michael D. West
;; APPLICANT: Jerry W. Shay
;; APPLICANT: Woodring E. Wright
;; APPLICANT: Elizabeth Blackburn
;; APPLICANT: Nam Woo Kim
;; APPLICANT: Calvin B. Harley
;; APPLICANT: Scott L. Weinrich
;; APPLICANT: Catherine Strahl
;; APPLICANT: Michael J. McEathern
;; APPLICANT: Homayoun Vaziri
;; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
;; TITLE OF INVENTION: CONDITIONS RELATED TO TELOMERE
;; TITLE OF INVENTION: LENGTH AND/OR TELOMERASE ACTIVITY
;; NUMBER OF SEQUENCES: 58
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Lyon & Lyon
;; STREET: 633 West Fifth Street
;; CITY: Suite 4700
;; CITY: Los Angeles
;; STATE: California
;; COUNTRY: U.S.A.
;; ZIP: 90071
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;; MEDIUM TYPE: storage
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: IBM P.C. DOS 5.0

;; SOFTWARE: FastSEQ Version 1.5
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/151,477A
;; FILING DATE: No. 5830644ember 12, 1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/038,766
;; FILING DATE: March 24, 1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Warburg, Richard
;; REGISTRATION NUMBER: 32,327
;; REFERENCE/DOCKET NUMBER: 202/189
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (213) 489-1600
;; TELEFAX: (213) 955-0440
;; TELEX: 67-3510
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 6
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; US-08-151-477A-4
Query Match 100.0%; Score 6; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.8e+07;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTAGGG 6
Db 6 TTAGGG 1
RESULT 6
US-08-670-999-3
;; Sequence 3, Application US/08670999
;; Patent No. 5849727
;; GENERAL INFORMATION:
;; APPLICANT: Porter, Thomas R.
;; APPLICANT: Iverson, Patrick L.
;; TITLE OF INVENTION: Compositions and Methods for Altering
;; TITLE OF INVENTION: the Biodistribution of Biological Agents
;; NUMBER OF SEQUENCES: 6
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Zarley, McKee, Thomte, Voorhees & Sease
;; STREET: 801 Grand Suite 3200
;; CITY: Des Moines
;; STATE: Iowa
;; COUNTRY: United States
;; ZIP: 50309
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC Compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/670,999
;; FILING DATE:
;; CLASSIFICATION: 514
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Nebel, Heidi S.
;; REGISTRATION NUMBER: 37,719
;; REFERENCE/DOCKET NUMBER: unmc 107A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 515-288-3667
;; TELEFAX: 515-288-1338
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 6 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: CDNA
;; HYPOTHETICAL: NO

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 6, 2003, 07:52:05 ; Search time 31.0714 Seconds
(without alignments)
59.220 Million cell updates/sec

Title: US-09-540-843-11
Perfect score: 6
Sequence: 1 ttaggg 6

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 558892

Minimum DB seq length: 0
Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2.6/ptodata/1/ina/5A-COMB.seq:*
2: /cgn2.6/ptodata/1/ina/5B-COMB.seq:*
3: /cgn2.6/ptodata/1/ina/6A-COMB.seq:*
4: /cgn2.6/ptodata/1/ina/6B-COMB.seq:*
5: /cgn2.6/ptodata/1/ina/PCTUS-COMB.seq:*
6: /cgn2.6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	6	100.0	6	1	US-08-381-097A-3
C 2	6	100.0	6	1	US-08-381-097A-5
C 3	6	100.0	6	1	US-08-153-051B-4
4	6	100.0	6	1	US-08-337-684-2
C 5	6	100.0	6	2	US-08-151-477A-4
6	6	100.0	6	2	US-08-670-999-3
7	6	100.0	6	3	US-08-729-598-4
8	6	100.0	6	3	US-08-819-867-9
C 9	6	100.0	6	3	US-08-819-867-27
10	6	100.0	6	3	US-08-630-019A-1
11	6	100.0	6	3	US-09-018-545-3
12	6	100.0	6	4	US-09-114-399-3
13	6	100.0	6	5	PCT-US96-01206-1
14	6	100.0	7	3	US-08-729-598-8
15	6	100.0	8	3	US-08-838-545-15
C 16	6	100.0	8	3	US-08-838-545-30
17	6	100.0	8	3	US-08-838-545-34
18	6	100.0	8	4	US-09-349-532-15
C 19	6	100.0	8	4	US-09-349-532-30
20	6	100.0	8	4	US-09-349-532-34
21	6	100.0	9	1	US-08-337-684-3
22	6	100.0	9	3	US-08-630-019A-27
23	6	100.0	9	3	US-09-069-434-14
24	6	100.0	9	3	US-08-838-545-16
25	6	100.0	9	4	US-09-349-532-16
26	6	100.0	10	1	US-08-192-300-18
27	6	100.0	10	2	US-08-531-743-10

28	6	100.0	10	3	US-08-630-019A-8	Sequence 8, Appli
29	6	100.0	10	3	US-08-838-545-7	Sequence 7, Appli
C 30	6	100.0	10	3	US-08-838-545-11	Sequence 11, Appl
31	6	100.0	10	3	US-08-838-545-17	Sequence 17, Appl
32	6	100.0	10	3	US-08-838-545-21	Sequence 21, Appl
C 33	6	100.0	10	3	US-08-838-545-29	Sequence 29, Appl
34	6	100.0	10	4	US-08-974-549A-527	Sequence 527, App
35	6	100.0	10	4	US-09-349-532-7	Sequence 7, Appli
C 36	6	100.0	10	4	US-09-349-532-11	Sequence 11, Appl
37	6	100.0	10	4	US-09-349-532-17	Sequence 17, Appl
38	6	100.0	10	4	US-09-349-532-21	Sequence 21, Appl
C 39	6	100.0	10	4	US-09-349-532-29	Sequence 29, Appl
C 40	6	100.0	11	1	US-08-330-123A-2	Sequence 2, Appli
C 41	6	100.0	11	1	US-08-482-115B-2	Sequence 2, Appli
C 42	6	100.0	11	2	US-08-660-678A-2	Sequence 11, Appl
43	6	100.0	11	2	US-08-531-743-11	Sequence 12, Appl
C 44	6	100.0	11	2	US-08-531-743-12	Sequence 12, Appl
C 45	6	100.0	11	2	US-08-485-778-36	Sequence 36, Appl

ALIGNMENTS

RESULT 1
US-08-381-097A-3
; Sequence 3, Application US/08381097A
; Patent No. 5643890
; GENERAL INFORMATION:
; APPLICANT: Iverson, Patrick L.
; APPLICANT: Mata, John E.
; TITLE OF INVENTION: Synthetic Oligodeoxyribonucleotides
; TITLE OF INVENTION: Which Mimic Telomeric Sequences for Use in the Treatment
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zarely, McKee, Thomte, Voorhees, & Sease
; STREET: 801 Grand Suite 3200
; CITY: Des Moines
; STATE: Iowa
; COUNTRY: United States
; ZIP: 50309
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08381,097A
; FILING DATE: 31-JAN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Nebel, Heidi S
; REGISTRATION NUMBER: 37,719
; REFERENCE/DOCKET NUMBER: unmc 63092
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 515-288-3667
; TELEFAX: 515-288-1338
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-381-097A-3

Query Match 100.0%; Score 6; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.8e+07;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1 TTAGGG 6

REFERENCE 1 (bases 1 to 21)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Other_ESTS: 2821108.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue procurement: DCTD/DPB cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
project clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
Scores: PHRED from University of Washington Genome Center. Vector
Trimming: cross match from University of Washington Genome Center
PHRAP suite. Poly-T identification: patmatch.pl from Berkeley
Drosophila Genome Project. University of Washington Genome Center:
<http://www.genome.washington.edu> Low Quality Sequence: 10
contiguous PHRED high quality bases followed vector sequence. Very
Low Quality Sequence: Trace file contained 21 contiguous distinct
peaks following vector sequence. Polyadenylation: Based upon the
presence of a xhoI site followed by a run of 14 or more T residues
at the beginning of the sequence, this cDNA insert was
polyadenylated.
Plate: LLCM5 row: P column: 5
High quality sequence stop: 10.
Location/Qualifiers
1. .21
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2821108"
/clone_lib="NIH MGC 7"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 4 a 6 c 0 g 11 t
ORIGIN

Query Match 100.0%; Score 6; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTAGGG 6
|||||
Db 20 TTAGGG 15

RESULT 15
LOCUS AZ331625/c 21 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0059M07R mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0059M07 R, DNA sequence.
ACCESSION AZ331625
VERSION AZ331625.1 GI:10394498
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Lonacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.
and Wright,D..Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: rdunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0059 row: M column: 07
Seq primer: CACACGAGAAACACGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
1. .21
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0059M07"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gil4732114[gb|AF129072.1]), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 8 a 7 c 0 g 6 t
ORIGIN

Query Match 100.0%; Score 6; DB 17; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTAGGG 6
|||||
Db 16 TTAGGG 11

Search completed: July 6, 2003, 09:39:51
Job time : 898.643 secs

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/organism="Trypanosoma brucei"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="158a03"

BASE COUNT      6 a      11 c      0 g      3 t
ORIGIN

Query Match      100.0%; Score 6; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TTAGGG 6
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Db      19 TTAGGG 14

RESULT 12
TA199G02Q/c
LOCUS      TA199G02Q      20 bp      DNA      linear      GSS 13-DEC-2000
DEFINITION      T. brucei sheared genomic DNA clone 199g02, reverse sequence,
                  genomic survey sequence.
ACCESSION      AL476798
VERSION      AL476798.1 GI:11843362
KEYWORDS      GSS.
SOURCE      Trypanosoma brucei.
ORGANISM      Eukaryota; Euzlenozoa; Kinetoplastida; Trypanosomatidae;
              Trypanosoma.
REFERENCE      1 (bases 1 to 20)
AUTHORS      Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
              Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
              Melville,S.E., Rajadream,M.A. and Barrell,B.G.
TITLE      Direct Submission
JOURNAL      Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
              project. Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
              Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
              nh@sanger.ac.uk
COMMENT      Constructed at the Institute for Genomic Research (TIGR),
              Rockville, MD. Genomic DNA isolated from a cloned population of
              Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
              to give a tight size distribution (
              4 kb). The v + i method used for the library construction is
              described in detail in Smith, H. and Venter, J.C. (Making small
              insert libraries for whole genome shotgun sequencing projects. In
              Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
              Barrell, Oxford University Press, 1999).
              Email: nelsayed@tigr.org
              Details of T. brucei sequencing at the Sanger Centre are available
              at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES
    source
        1..20
            Location/Qualifiers
                /organism="Trypanosoma brucei"
                /strain="TREU927"
                /db_xref="taxon:5691"
                /clone="199g02"
                3 g      8 t

BASE COUNT      5 a      4 c      3 g
ORIGIN

Query Match      100.0%; Score 6; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TTAGGG 6
        |||||
Db      20 TTAGGG 15

RESULT 13
AW248826/c
LOCUS      AW248826      21 bp      mRNA      linear      EST 07-JAN-2000
DEFINITION      2821056.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821056 3',
                  mRNA sequence.
ACCESSION      AW248826

/organism="Trypanosoma brucei"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="158a03"

BASE COUNT      6 a      11 c      0 g      3 t
ORIGIN

Query Match      100.0%; Score 6; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TTAGGG 6
        |||||
Db      20 TTAGGG 15

BASE COUNT      4 a      3 c      3 g      11 t
ORIGIN

Query Match      100.0%; Score 6; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TTAGGG 6
        |||||
Db      20 TTAGGG 15

RESULT 14
AW248836/c
LOCUS      AW248836      21 bp      mRNA      linear      EST 07-JAN-2000
DEFINITION      2821108.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821108 3',
                  mRNA sequence.
ACCESSION      AW248836
VERSION      AW248836.1 GI:6591829
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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AW248826.1 GI:6591819
EST.
SOURCE      human.
ORGANISM      Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 21)
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL      National Institutes of Health, Mammalian Gene Collection (MGC)
              Unpublished (1999)
COMMENT      Other_ESTs: 2821056.5prime
              Contact: Robert Strausberg, Ph.D.
              Email: cgapbs-r@mail.nih.gov
              Tissue Procurement: DCTD/DTF cDNA Library Preparation: Ling
              Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
              Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
              project Clone distribution: MGC clone distribution information can
              be found through the I.M.A.G.E. Consortium/LLNL at:
              www-bio.lnl.gov/bbrp/image/image.html Base Calling / Quality
              Scores: PHRED from University of Washington Genome Center. Vector
              Trimming: cross_match from University of Washington Genome Center
              PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
              Drosophila Genome Project. University of Washington Genome Center:
              http://www.genome.washington.edu Low Quality Sequence: 21
              contiguous PHRED high quality bases following vector sequence. Very
              Low Quality Sequence: Trace file contained 21 contiguous distinct
              peaks following vector sequence. Polyadenylation: Based upon the
              presence of a XhoI site followed by a run of 14 or more T residues
              at the beginning of the sequence, this cDNA insert was
              polyadenylated.
              Plate: LICM5 row: N column: 1
              High quality sequence stop: 21.
              Location/Qualifiers
                1..21
                    /organism="Homo sapiens"
                    /db_xref="taxon:9606"
                    /clone="IMAGE:2821056"
                    /clone_lib="NIH_MGC_7"
                    /tissue_type="small cell carcinoma"
                    /cell_line="MGC3"
                    /lab_host="DH10B (phage-resistant)"
                    /note="Organ: lung; Vector: pORB7; Site_1: XhoI; Site_2:
                    EcoRI; cDNA made by oligo-df priming. Directionally
                    cloned into EcoRI/XhoI sites using the following 5'
                    adaptor: GGCACGAG(G). Size-selected >500bp for average
                    insert size 1.8kb. Library constructed by Ling Hong in
                    the laboratory of Gerald M. Rubin (University of
                    California, Berkeley) using ZAP-cDNA synthesis kit
                    (Stratagene) and Superscript II RT (Life Technologies)."
                4 a      3 c      3 g      11 t
                    Location/Qualifiers
                        Query Match      100.0%; Score 6; DB 10; Length 21;
                        Best Local Similarity 100.0%; Pred. No. 4.5e+05;
                        Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TTAGGG 6
        |||||
Db      20 TTAGGG 15

RESULT 14
AW248836/c
LOCUS      AW248836      21 bp      mRNA      linear      EST 07-JAN-2000
DEFINITION      2821108.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821108 3',
                  mRNA sequence.
ACCESSION      AW248836
VERSION      AW248836.1 GI:6591829
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0071D09"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT      2 a      2 c      10 g      6 t
ORIGIN

```

```

Query Match      100.0%; Score 6; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 TTAGGG 6
        |||||
Db      6 TTAGGG 11

```

```

RESULT 10
AZ960008/c
LOCUS      20 bp      DNA      linear      GSS 27-APR-2001
DEFINITION      2M027G21R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M027G21 R, DNA sequence.
ACCESSION      AZ960008
VERSION      AZ960008.1 GI:13831235
KEYWORDS      GSS.
SOURCE      house mouse.
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0227 row: G column: 21
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
FEATURES
Location/Qualifiers
1..20
source

```

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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M027G21"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, Tl-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT      8 a      5 c      2 g      5 t
ORIGIN

```

```

Query Match      100.0%; Score 6; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 TTAGGG 6
        |||||
Db      18 TTAGGG 13

```

```

RESULT 11
TA158A03P/c
LOCUS      20 bp      DNA      linear      GSS 13-DEC-2000
DEFINITION      T. brucei sheared genomic DNA clone 158a03, forward sequence,
genomic survey sequence.
ACCESSION      AL472050
VERSION      AL472050.1 GI:11837404
KEYWORDS      GSS.
SOURCE      Trypanosoma brucei.
ORGANISM      Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
1 (bases 1 to 20)
Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Meiville,S.E., Rajandream,M.A. and Barrell,B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T-brucei/.
FEATURES
Location/Qualifiers
1..20
source

```

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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0467010"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT      5 a      2 c      7 g      6 t
ORIGIN

```

```

Query Match      100.0%; Score 6; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 TTAGGG 6
        |||||
Db      13 TTAGGG 18

```

```

RESULT 8
AZ662909
LOCUS      20 bp      DNA      linear      GSS 14-DEC-2000
DEFINITION 1M0542617F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0542617 F, DNA sequence.
ACCESSION  AZ662909
VERSION     AZ662909.1 GI:11800055
KEYWORDS    GSS.
SOURCE      house mouse.
ORGANISM    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

```

```

REFERENCE   1 (bases 1 to 20)
AUTHORS     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL     Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0542 row: G column: 17
            Seq primer: CGTTGTAACGACGCCAGT
            Class: plasmid ends
            High quality sequence stop: 20.

```

```

FEATURES             source
                    1..20

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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0542617"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT      2 a      2 c      11 g      5 t
ORIGIN

```

```

Query Match      100.0%; Score 6; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 TTAGGG 6
        |||||
Db      7 TTAGGG 12

```

```

RESULT 9
AZ808291
LOCUS      20 bp      DNA      linear      GSS 20-FEB-2001
DEFINITION 2M0071D09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0071D09 R, DNA sequence.
ACCESSION  AZ808291
VERSION     AZ808291.1 GI:12973320
KEYWORDS    GSS.
SOURCE      house mouse.
ORGANISM    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

```

```

REFERENCE   1 (bases 1 to 20)
AUTHORS     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL     Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0071 row: D column: 09
            Seq primer: CACACAGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 20.

```

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FEATURES             source
                    1..20

```

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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0080J04"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT      8 a  6 c  2 g  3 t
ORIGIN

```

```

Query Match      100.0%; Score 6; DB 17; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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QY      1 TTAGGG 6
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Db      17 TTAGGG 12

```

```

RESULT 6
LOCUS      AZ345513/C
DEFINITION IM0080J04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0080J04 F, DNA sequence.
ACCESSION  AZ345513
VERSION     AZ345513.1 GI:10424750
KEYWORDS   GSS.
SOURCE     house mouse.
ORGANISM   Mus musculus
REFERENCE  1 (bases 1 to 20)
AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL    Unpublished (2000)
COMMENT    Contact: Robert B. Weiss
            University of Utah Genome Center
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0080 row: J column: 04
            Seq primer: CGTTGTAACAGCGCCAGT
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES   Location/Qualifiers
            source          1. .20

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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0080J04"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT      3 a  13 c  0 g  4 t
ORIGIN

```

```

Query Match      100.0%; Score 6; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 TTAGGG 6
        |||||
Db      16 TTAGGG 11

```

```

RESULT 7
LOCUS      AZ627174
DEFINITION IM0467010R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0467010 R, DNA sequence.
ACCESSION  AZ627174
VERSION     AZ627174.1 GI:11749364
KEYWORDS   GSS.
SOURCE     house mouse.
ORGANISM   Mus musculus
REFERENCE  1 (bases 1 to 20)
AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL    Unpublished (2000)
COMMENT    Contact: Robert B. Weiss
            University of Utah Genome Center
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0467 row: 0 column: 10
            Seq primer: CACACAGGAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES   Location/Qualifiers
            source          1. .20

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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCLM0200F10"
/clone.lib="Mouse 10kb plasmid UUGCLM library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT      7 a      2 g      5 t
ORIGIN

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Query Match      100.0%; Score 6; DB 17; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 TTAGGG 6
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Db       8 TTAGGG 3

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RESULT 4
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LOCUS      A2614760          19 bp      DNA      linear      GSS 13-DEC-2000
DEFINITION 1M0443A17R Mouse 10kb plasmid UUGCLM library Mus musculus genomic
clone UUGCLM0443A17 R, DNA sequence.
ACCESSION  A2614760
VERSION     A2614760.1  GI:11736950
KEYWORDS    GSS.
SOURCE      house mouse.
ORGANISM    Mus musculus

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REFERENCE   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS     Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 19)
            Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D., Weiss,R.

```

```

TITLE       Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL      Unpublished (2000)
COMMENT      Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0443 row: A column: 17
            Seq primer: CACACAGGAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES     Location/Qualifiers
            1..19
source

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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCLM0443A17"
/clone.lib="Mouse 10kb plasmid UUGCLM library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT      3 a      0 c      10 g      6 t
ORIGIN

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Query Match      100.0%; Score 6; DB 17; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 TTAGGG 6
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Db       4 TTAGGG 9

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RESULT 5
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DEFINITION 2M0102N07R Mouse 10kb plasmid UUGCLM library Mus musculus genomic
clone UUGC2M0102N07 R, DNA sequence.
ACCESSION  A2826736
VERSION     A2826736.1  GI:12996644
KEYWORDS    GSS.
SOURCE      house mouse.
ORGANISM    Mus musculus

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REFERENCE   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS     Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 19)
            Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D., Weiss,R.

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TITLE       Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL      Unpublished (2000)
COMMENT      Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0102 row: N column: 07
            Seq primer: CACACAGGAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES     Location/Qualifiers
            1..19
source

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http://www.genome.washington.edu Low Quality Sequence: 15
contiguous PHRED high quality bases following vector sequence. Very
Low Quality Sequence: Trace file contained 16 contiguous distinct
peaks following vector sequence. Polyadenylation: Based upon the
presence of a XhoI site followed by a run of 14 or more T residues
at the beginning of the sequence, this cDNA insert was
polyadenylated.

Plate: L1C01 row: K column: 7
High quality sequence stop: 15.

FEATURES

Location/Qualifiers
1. .16
/organism="Homo sapiens"
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/clone="IMAGE:2819454"
/clone_lib="NIH_MGC_7"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCAGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 3 a 0 c 3 g 10 t
ORIGIN

Query Match 100.0%; Score 6; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.2e+05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTAGGG 6
Db 9 TTAGGG 14

RESULT 2

AZ392246

LOCUS

DEFINITION AZ392246 19 bp DNA linear GSS 03-OCT-2000
IM0154612R Mouse 10kb plasmid UUGCLM library Mus musculus genomic
clone UUGCLM0154G12 R, DNA sequence.

ACCESSION AZ392246

VERSION AZ392246.1

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 19)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
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Plate: 0154 row: G column: 12
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES

Location/Qualifiers

1. .19

source

/organism="Mus musculus"
/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGCLM0154G12"

/clone_lib="Mouse 10kb plasmid UUGCLM library"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: pWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 3 a 5 c 5 g 6 t
ORIGIN

Query Match 100.0%; Score 6; DB 17; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.4e+05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTAGGG 6
Db 14 TTAGGG 19

RESULT 3

AZ422271/c

LOCUS

DEFINITION AZ422271 19 bp DNA linear GSS 03-OCT-2000
IM0200F10R Mouse 10kb plasmid UUGCLM library Mus musculus genomic
clone UUGCLM0200F10 R, DNA sequence.

ACCESSION AZ422271

VERSION AZ422271.1

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 19)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0200 row: F column: 10
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES

Location/Qualifiers

1. .19

source

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 6, 2003, 07:33:45 ; Search time 894.643 Seconds
(without alignments)
108.616 Million cell updates/sec

Title: US-09-540-843-11
Perfect score: 6
Sequence: 1 ttaggg 6

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 60474

Minimum DB seq length: 0
Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_othr:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	6	100.0	19	17	AZ392246
3	6	100.0	19	17	AZ422271
4	6	100.0	19	17	AZ614760
5	6	100.0	19	17	AZ826736
6	6	100.0	20	17	AZ345513

6	100.0	20	17	AZ627174	AZ627174
6	100.0	20	17	AZ662909	1M0467010
6	100.0	20	17	AZ808291	1M0542617
6	100.0	20	17	AZ960008	2M0071D09
6	100.0	20	17	TA158A03P	AZ960008
6	100.0	20	17	TA199G02Q	2M0227G21
6	100.0	21	10	AW248826	AL472050
6	100.0	21	10	AW248836	T. brucei
6	100.0	21	10	AW248836	2821056.3
6	100.0	21	10	AW248836	2821108.3
6	100.0	21	17	AZ331625	AW248836
6	100.0	21	17	AZ399400	AZ331625
6	100.0	21	17	AZ445481	1M0059M07
6	100.0	21	17	AZ626594	AZ399400
6	100.0	21	17	AZ626594	1M0165C13
6	100.0	21	17	AZ760907	AZ445481
6	100.0	21	17	AZ766315	1M0241P15
6	100.0	21	17	AZ828389	AZ626594
6	100.0	21	17	AZ833919	1M0466J20
6	100.0	21	17	AZ877328	AZ760907
6	100.0	22	9	AA954126	1M0554P21
6	100.0	22	9	AA527213	AZ766315
6	100.0	22	14	D18745	1M0563K14
6	100.0	22	17	AZ324747	AZ828389
6	100.0	22	17	AZ464647	2M0105P16
6	100.0	22	17	AZ483833	AZ833919
6	100.0	22	17	AZ500414	2M0116N18
6	100.0	22	17	AZ598320	AZ877328
6	100.0	22	17	AZ629501	2M0192C18
6	100.0	22	17	AZ666649	AA954126
6	100.0	22	17	AZ836104	AA527213
6	100.0	22	17	AZ855118	D18745
6	100.0	22	17	AZ858772	AZ324747
6	100.0	23	9	AU258772	AZ464647
6	100.0	23	17	AZ423815	AZ483833
6	100.0	23	17	AZ465280	6
6	100.0	23	17	AZ623979	100.0
6	100.0	23	17	AZ817008	22
6	100.0	23	17	AZ979817	100.0
6	100.0	23	17	BH857265	22
6	100.0	23	17	AZ309633	100.0
6	100.0	24	17	AZ785628	22
6	100.0	24	17	AZ806300	100.0

ALIGNMENTS

RESULT 1
AW248958
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AW248958 16 bp mRNA linear EST 07-JAN-2000
2819454.3prime NTH_MGC_7 Homo sapiens cDNA clone IMAGE:2819454 3',
mRNA sequence.
AW248958 1 GI:6591951
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgc.nci.nih.gov/
1 (bases 1 to 16)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Other_ESTS: 2819454.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov

Tissue Procurement: DCTD/DPF CDNA Library Preparation: Ling
Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LLNL) DNA Sequencing by: Berkeley MGC Sequencing
Project Clone Distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
Scores: PHRED from University of Washington Genome Center. Vector
Trimming: cross_match from University of Washington Genome Center
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
Drosophila Genome Project. University of Washington Genome Center:

Query Match 100.0%; Score 6; DB 6; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.9e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTAA 6
 Db 6 CCCTAA 1

RESULT 14
 AR016034
 LOCUS AR016034 11 bp DNA linear PAT 05-DEC-1998

DEFINITION Sequence 2 from patent US 5776679.
 ACCESSION AR016034
 VERSION AR016034.1 GI:3972311

KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 11)
 AUTHORS Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
 TITLE Assays for the DNA component of human telomerase
 JOURNAL Patent: US 5776679-A 2 07-JUL-1998;

FEATURES
 source Location/Qualifiers
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BASE COUNT 4 a 5 c 0 g 2 t
 ORIGIN

Query Match 100.0%; Score 6; DB 6; Length 11;
 Best Local Similarity 100.0%; Pred. No. 3.8e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 5 CCCTAA 10

RESULT 15
 AR026486/c
 LOCUS AR026486 11 bp DNA linear PAT 29-SEP-1999

DEFINITION Sequence 11 from patent US 5856096.
 ACCESSION AR026486

VERSION AR026486.1 GI:5937326

KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 11)
 AUTHORS Windle,B.E., Qiu,M., Chen,S.-F., Fletcher,T.M. and Maine,I.
 TITLE Rapid and sensitive assays for detecting and distinguishing between
 progressive and non-processive telomerase activities
 JOURNAL Patent: US 5856096-A 11 05-JAN-1999;

FEATURES
 source Location/Qualifiers
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BASE COUNT 2 a 0 c 5 g 4 t
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Query Match 100.0%; Score 6; DB 6; Length 11;
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QY 1 CCCTAA 6
 Db 7 CCCTAA 2

Search completed: July 6, 2003, 08:29:51
 Job time : 285 secs


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Query Match      100.0%; Score 6; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.9e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTAA 6
Db 3 CCCTAA 8

RESULT 11
LOCUS AX153524 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 1439 from Patent WO0138577.
ACCESSION AX153524
VERSION AX153524.1 GI:14535175
KEYWORDS human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 10)
Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
Human transcriptomes
Patent: WO 0138577-A 1439 31-MAY-2001;
The Johns Hopkins University (US)
LOCATION/Qualifiers
1. .10
/organism="Homo sapiens"
/db_xref="taxon:9606"
3 t

BASE COUNT      1 a      1 c      5 g      3 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 3.9e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTAA 6
Db 10 CCCTAA 5

RESULT 12
LOCUS BD011231 10 bp DNA linear PAT 31-JAN-2002
DEFINITION Human telomerase catalytic subunit.
ACCESSION BD011231
VERSION BD011231.1 GI:18639604
KEYWORDS JP 2001081042-A/188.
SOURCE unidentified.
ORGANISM unclassified.
1 (bases 1 to 10)
Sechi,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Mori,G.B.,
Harley,C.B. and Andrews,W.H.
Human telomerase catalytic subunit
Patent: JP 2001081042-A 188 27-MAR-2001;
GERON CORP.,UNIVERSITY TECHNOLOGY CORP
OS unidentified
PN JP 2001081042-A/188
PD 27-MAR-2001
PF 27-JUL-2000 JP 2000227474
PR 01-OCT-1996 US 08/724643,18-APR-1997 US 08/844419 PR
23-APR-1997 US 08/846017,06-MAY-1997 US 08/851843 PR
09-MAY-1997 US 08/854050,14-AUG-1997 US 08/911312 PR
14-AUG-1997 US 08/912951,14-AUG-1997 US 08/915503 PI THOMAS
R SECHI,JOACHIM LINGNER,TORU NAKAMURA,KAREN B CHAPMAN, PI GREG B
MORIN,
PI CALVIN B HARLEY,WILLIAM H ANDREWS
PC A61K38/00,A61K31/7088,A61K39/00,A61K48/00,A61P35/00,A61P43/00,
PC C07K5/10,

BASE COUNT      5 a      3 c      0 g      2 t
ORIGIN

Query Match      100.0%; Score 6; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.9e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTAA 6
Db 6 CCCTAA 1

RESULT 13
LOCUS E36980 10 bp DNA linear PAT 18-JUN-2001
DEFINITION Human telomerase catalytic subunit promoter.
ACCESSION E36980
VERSION E36980.1 GI:13022943
KEYWORDS JP 1999253177-A/188.
SOURCE unidentified.
ORGANISM unclassified.
1 (bases 1 to 10)
Thomas,R.S., Jochimu,R., Toru,N., Karen,B.C., Greg,B.M.,
Calvin,B.H. and William,H.A.
Human telomerase catalytic subunit promoter
Patent: JP 1999253177-A 188 21-SEP-1999;
JERON CORP,UNIVERSITY TECHNOLOGY CORP
OS unidentified
PN JP 1999253177-A/188
PD 21-SEP-1999
PF 15-OCT-1998 JP 1998320169
PR 01-OCT-1996 US 08/724,643,18-APR-1997 US 08/844,419, PR
25-APR-1997 US 08/846,017,06-MAY-1997 US 08/851,843, PR
09-MAY-1997 US 08/854,050,14-AUG-1997 US 08/911,312, PR
14-AUG-1997 US 08/912,951,14-AUG-1997 US 08/915,503 PI THOMAS
R SECHI,JOCHIMU RINGNER,TORU NAKAMURA,KAREN B CHAPMAN, PI GREG B
MORIN
PI CALVIN B HAREI,WILLIAM H ANDREWS
PC C12N15/09,A61K31/770,A61K38/55,A61K39/395,A61K48/00,
PC C12Q1/02,
PC C12Q1/48,C12Q1/68,G01N33/15,G01N33/48,G01N33/50//C07K14/47, PC
C07K16/40,
PC C12N1/19,C12N1/21,C12N5/10,C12N9/12,C12P21/08,(C12N1/19, PC
C12R1:84),
PC (C12N1/21,C12R1:19),(C12N9/12,C12R1:19),(C12N9/12,C12R1:84),
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FH Key Location/Qualifiers
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Query Match      100.0%; Score 6; DB 6; Length 10;
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Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTAA 6
Db 6 CCCTAA 1

RESULT 13
LOCUS E36980/c
DEFINITION Human telomerase catalytic subunit promoter.
ACCESSION E36980
VERSION E36980.1 GI:13022943
KEYWORDS JP 1999253177-A/188.
SOURCE unidentified.
ORGANISM unclassified.
1 (bases 1 to 10)
Thomas,R.S., Jochimu,R., Toru,N., Karen,B.C., Greg,B.M.,
Calvin,B.H. and William,H.A.
Human telomerase catalytic subunit promoter
Patent: JP 1999253177-A 188 21-SEP-1999;
JERON CORP,UNIVERSITY TECHNOLOGY CORP
OS unidentified
PN JP 1999253177-A/188
PD 21-SEP-1999
PF 15-OCT-1998 JP 1998320169
PR 01-OCT-1996 US 08/724,643,18-APR-1997 US 08/844,419, PR
25-APR-1997 US 08/846,017,06-MAY-1997 US 08/851,843, PR
09-MAY-1997 US 08/854,050,14-AUG-1997 US 08/911,312, PR
14-AUG-1997 US 08/912,951,14-AUG-1997 US 08/915,503 PI THOMAS
R SECHI,JOCHIMU RINGNER,TORU NAKAMURA,KAREN B CHAPMAN, PI GREG B
MORIN
PI CALVIN B HAREI,WILLIAM H ANDREWS
PC C12N15/09,A61K31/770,A61K38/55,A61K39/395,A61K48/00,
PC C12Q1/02,
PC C12Q1/48,C12Q1/68,G01N33/15,G01N33/48,G01N33/50//C07K14/47, PC
C07K16/40,
PC C12N1/19,C12N1/21,C12N5/10,C12N9/12,C12P21/08,(C12N1/19, PC
C12R1:84),
PC (C12N1/21,C12R1:19),(C12N9/12,C12R1:19),(C12N9/12,C12R1:84),
PC (C12N9/12,C12R1:91),C12N15/00,A61K37/64,C12N5/00 CC
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CC Topology: Linear;
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BASE COUNT      2 a      0 c      4 g      4 t
ORIGIN
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RESULT 6
LOCUS AR026485 10 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 10 from patent US 5856096.
ACCESSION AR026485
VERSION AR026485.1 GI:5937325
KEYWORDS
SOURCE unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Windle,B.E., Qiu,M., Chen,S.-F., Fletcher,T.M. and Maine,I.
TITLE Rapid and sensitive assays for detecting and distinguishing between
JOURNAL processive and non-processive telomerase activities
FEATURES Patent: US 5856096-A 10 05-JAN-1999;
source Location/Qualifiers
1. .10
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BASE COUNT 2 a 0 c 4 g 4 t
ORIGIN

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Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTAA 6
Db 6 CCCTAA 1

RESULT 7
AX152177/c
LOCUS AX152177 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 92 from Patent WO0138577.
ACCESSION AX152177
VERSION AX152177.1 GI:14533828
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 92 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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Best Local Similarity 100.0%; Pred. No. 3.9e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTAA 6
Db 7 CCCTAA 2

RESULT 8
AX153381
LOCUS AX153381 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 1296 from Patent WO0138577.
ACCESSION AX153381
VERSION AX153381.1 GI:14535032
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 10)
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 1296 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES Location/Qualifiers
1. .10
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 5 a 3 c 0 g 2 t
ORIGIN

Query Match 100.0%; Score 6; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.9e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTAA 6
Db 3 CCCTAA 8

RESULT 9
AX153382
LOCUS AX153382 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 1297 from Patent WO0138577.
ACCESSION AX153382
VERSION AX153382.1 GI:14535033
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 1297 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES Location/Qualifiers
1. .10
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 5 a 3 c 0 g 2 t
ORIGIN

Query Match 100.0%; Score 6; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.9e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTAA 6
Db 3 CCCTAA 8

RESULT 10
AX153383
LOCUS AX153383 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 1298 from Patent WO0138577.
ACCESSION AX153383
VERSION AX153383.1 GI:14535034
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 1298 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES Location/Qualifiers
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/db_xref="taxon:9606"

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  /note="synthetic primer"
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  2 a 3 c 0 g 1 t
BASE COUNT
ORIGIN

Query Match
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Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTAA 6
Db 1 CCCCC 6

RESULT 2
AX058275/c
LOCUS AX058275 6 bp DNA linear PAT 17-JAN-2001
DEFINITION Sequence 10 from Patent WO0074667.
ACCESSION AX058275
VERSION AX058275.1 GI:12310774
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Au,J.L. and Wientjes,G.
TITLE Compositions active in telomere damage comprising a taxane and telomerase inhibitor
JOURNAL Patent: WO 0074667-A 10 14-DEC-2000;
Au, Jessie L.S. (US); Wientjes, Guillaume (US)
FEATURES
source
  /organism="synthetic construct"
  /db_xref="taxon:32630"
  /note="primer/probe"
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BASE COUNT
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 6; DB 6; Length 6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTAA 6
Db 6 CCCCC 1

RESULT 3
AX175285/c
LOCUS AX175285 6 bp DNA linear PAT 03-JUL-2001
DEFINITION Sequence 49 from Patent WO0144465.
ACCESSION AX175285
VERSION AX175285.1 GI:14598653
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Phillips,N.C. and Fillon,M.C.
TITLE Therapeutically useful synthetic oligonucleotides
JOURNAL Patent: WO 0144465-A 49 21-JUN-2001;
Bioniche Life Sciences Inc. (CA)
FEATURES
source
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  /db_xref="taxon:32630"
  1..6
  1 a 0 c 3 g 2 t
BASE COUNT
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 6; DB 6; Length 6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTAA 6
Db 6 CCCCC 1

RESULT 4
AX268763/c
LOCUS AX268763 6 bp DNA linear PAT 29-OCT-2001
DEFINITION Sequence 11 from Patent WO0174342.
ACCESSION AX268763
VERSION AX268763.1 GI:16541835
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Gilchrist,B.A., Yaar,M. and Eller,M.
TITLE Use of locally applied dna fragments
JOURNAL Patent: WO 0174342-A 11 11-OCT-2001;
TRUSTEES OF BOSTON UNIVERSITY (US)
LOCATION/Qualifiers
FEATURES
source
  /organism="synthetic construct"
  /db_xref="taxon:32630"
  /note="Synthetic DNA Fragment"
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  1 a 0 c 3 g 2 t
BASE COUNT
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 6; DB 6; Length 6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTAA 6
Db 6 CCCCC 1

RESULT 5
AX268764
LOCUS AX268764 6 bp DNA linear PAT 29-OCT-2001
DEFINITION Sequence 12 from Patent WO0174342.
ACCESSION AX268764
VERSION AX268764.1 GI:16541836
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Gilchrist,B.A., Yaar,M. and Eller,M.
TITLE Use of locally applied dna fragments
JOURNAL Patent: WO 0174342-A 12 11-OCT-2001;
TRUSTEES OF BOSTON UNIVERSITY (US)
LOCATION/Qualifiers
FEATURES
source
  /organism="synthetic construct"
  /db_xref="taxon:32630"
  /note="Synthetic DNA Fragment"
  1..6
  2 a 3 c 0 g 1 t
BASE COUNT
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 6; DB 6; Length 6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTAA 6
Db 1 CCCCC 6
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 6, 2003, 06:42:31 ; Search time 285 Seconds
(without alignments)
612.691 Million cell updates/sec

Title: US-09-540-843-12
Perfect score: 6
Sequence: 1 cccaa 6

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 774614

Minimum DB seq length: 0
Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*

1: gb_ba:*
2: gb_htg:*
3: gb_in:*
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5: gb_ov:*
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7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
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24: em_ph:*
25: em_pl:*
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32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rtd:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	6	100.0	6	6	AX055801	AX055801 Sequence
c 2	6	100.0	6	6	AX058275	AX058275 Sequence
c 3	6	100.0	6	6	AX175285	AX175285 Sequence
c 4	6	100.0	6	6	AX268763	AX268763 Sequence
5	6	100.0	6	6	AX268764	AX268764 Sequence
c 6	6	100.0	10	6	AR026485	AR026485 Sequence
c 7	6	100.0	10	6	AR026485	AR026485 Sequence
8	6	100.0	10	6	AX152177	AX152177 Sequence
9	6	100.0	10	6	AX153381	AX153381 Sequence
10	6	100.0	10	6	AX153382	AX153382 Sequence
c 11	6	100.0	10	6	AX153383	AX153383 Sequence
c 12	6	100.0	10	6	AX153524	AX153524 Sequence
c 13	6	100.0	10	6	BD011231	BD011231 Human tel
c 14	6	100.0	10	6	E36980	E36980 Human telom
c 15	6	100.0	11	6	AR016034	AR016034 Sequence
16	6	100.0	11	6	AR026486	AR026486 Sequence
17	6	100.0	11	6	AR026487	AR026487 Sequence
18	6	100.0	11	6	AR059195	AR059195 Sequence
19	6	100.0	11	6	AR075506	AR075506 Sequence
20	6	100.0	11	6	AR161904	AR161904 Sequence
c 21	6	100.0	11	6	AX033373	AX033373 Sequence
c 22	6	100.0	11	6	AX268757	AX268757 Sequence
c 23	6	100.0	11	6	AX268761	AX268761 Sequence
c 24	6	100.0	11	6	AX283296	AX283296 Sequence
c 25	6	100.0	11	6	AX394462	AX394462 Sequence
c 26	6	100.0	11	6	AX394499	AX394499 Sequence
27	6	100.0	11	6	AX471710	AX471710 Sequence
28	6	100.0	11	6	BD003369	BD003369 Mammalian
29	6	100.0	12	6	I31749	I31749 Sequence 2
30	6	100.0	12	6	A21302	A21302 Nucleotide
c 31	6	100.0	12	6	AR026476	AR026476 Sequence
c 32	6	100.0	12	6	AR026477	AR026477 Sequence
c 33	6	100.0	12	6	AR026480	AR026480 Sequence
c 34	6	100.0	12	6	AR050933	AR050933 Sequence
c 35	6	100.0	12	6	AR050938	AR050938 Sequence
c 36	6	100.0	12	6	AR059223	AR059223 Sequence
c 37	6	100.0	12	6	AR059544	AR059544 Sequence
c 38	6	100.0	12	6	AR059545	AR059545 Sequence
c 39	6	100.0	12	6	AR075547	AR075547 Sequence
40	6	100.0	12	6	AR134878	AR134878 Sequence
c 41	6	100.0	12	6	AR134879	AR134879 Sequence
c 42	6	100.0	12	6	AR193363	AR193363 Sequence
c 43	6	100.0	12	6	AR200885	AR200885 Sequence
c 44	6	100.0	12	6	AR204552	AR204552 Sequence
c 45	6	100.0	12	6	AR204553	AR204553 Sequence

ALIGNMENTS

RESULT 1
AX055801
LOCUS
DEFINITION Sequence 5 from Patent WO0073420.
ACCESSION AX055801
VERSION AX055801.1 GI:12228914
KEYWORDS synthetic construct,
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 6)
AUTHORS Hahn,W.C. and Weinberg,R.A.
TITLE Creation of human tumorigenic cells and uses therefor
JOURNAL Patent: WO 0073420-A 5 07-DEC-2000;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; DANA-FARBER


```
QY      1 CCCTAA 6
Db      7 CCCTAA 2

RESULT 14
AAT05735/c
ID      AAT05735 standard; DNA; 9 BP.
XX
XX
AC      AAT05735;
XX
XX      01-FEB-1996 (first entry)
XX
XX      Telomerase oligonucleotide substrate #2.
DE
XX      Telomerase; proliferation; telomere; hybrid; immortalised cell; anaemia;
KW      transplantation; cell therapy; treatment; AIDS; leukaemia; lymphoma; ss.
XX
XX      Synthetic.
OS
XX      W09513383-AL.
PN
XX      18-MAY-1995.
PD
XX      10-NOV-1994; 94WO-US13130.
PF
XX      12-NOV-1993; 93US-0153051.
PR
XX      12-NOV-1993; 93US-0151477.
XX
XX      (GERO-) GERON CORP.
PA
XX      (TEXA ) UNIV TEXAS SYSTEM.
XX
XX      Shay J, West MD, Wright WE;
PI
XX      WPI; 1995-224051/29.
DR
XX      Increasing telomere length in cells - to increase proliferative
PT      capacity and therefore delay cellular senescence, useful in cell
PT      therapy and transplantation
XX
XX      Claim 12; Page 29; 38pp; English.
PS
XX      Oligonucleotides AAT05734-7 are examples of telomerase substrates used
CC      to increase the proliferative capacity of normal cells that express
CC      telomerase activity. The oligonucleotides allow an increase in
CC      length of telomeres in normal cells and in hybrids of normal and
CC      immortalised cells. The increase in telomere length extends the
CC      capacity of cells to replicate, esp. those treated ex vivo and used
CC      for transplantation techniques e.g. cell therapy, for the treatment
CC      of AIDS, anaemia, leukaemia or lymphoma.
XX
XX      Sequence 9 BP; 2 A; 0 C; 3 G; 4 T; 0 other;

Query Match      100.0%; Score 6; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.4e+08;
Matches      6; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      1 CCCTAA 6
Db      6 CCCTAA 1

RESULT 15
AAT89240/c
ID      AAT89240 standard; DNA; 9 BP.
XX
XX
AC      AAT89240;
XX
XX      12-MAY-1998 (first entry)
DT
XX      Peptide nucleic acid 15, targeted to mammalian telomerase.
DE
XX      Peptide nucleic acid; PNA; cancer; telomerase; probe; hybridisation;
KW
```

```
inhibitor; ss.
KW
XX      Synthetic.
OS
XX
XX      Location/Qualifiers
FH      1..9
FT      /*tag= a
FT      /note= "Sugar-phosphate backbone has been replaced by
FT      a peptide backbone"
XX
XX      W09738013-AL.
PN
XX      16-OCT-1997.
PD
XX      09-APR-1997; 97WO-US05931.
PF
XX      09-APR-1996; 96US-0630019.
PR
XX      (GERO-) GERON CORP.
XX
XX      Corey D, Norton JC, Piatyszek MA, Shay JW, Wright WE;
PI
XX      WPI; 1997-512647/47.
DR
XX
XX      New peptide nucleic acids hybridising to mammalian telomerase RNA -
PT      used to inhibit telomerase, for treating tumours and other
PT      proliferative diseases, also for diagnosis
XX
XX      Claim 9; Page 59; 76pp; English.
PS
XX
XX      This sequence is a novel peptide nucleic acid (PNA), which acts as
CC      an inhibitor of mammalian, preferably human, telomerase. The PNAs
CC      hybridise specifically to an RNA component of mammalian telomerase,
CC      and include the sequence GGG for specific hybridisation to the template
CC      region of this component. PNAs can be used as probes to detect the
CC      RNA component of mammalian telomerase and as inhibitors of telomerase
CC      activity, especially in the treatment of cancer.
XX
XX      Sequence 9 BP; 2 A; 0 C; 4 G; 3 T; 0 other;

Query Match      100.0%; Score 6; DB 18; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.4e+08;
Matches      6; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      1 CCCTAA 6
Db      8 CCCTAA 3

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Job time : 133.107 secs
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OS Synthetic.

XX Key Location/Qualifiers

PH modified_base 1..8

FT /*tag= a

FT /note= "This sequence is a peptide nucleic acid, i.e. it

FT contains a polyamide backbone instead of a

FT deoxyribose backbone"

XX

XX US6294650-B1.

XX

XX 25-SEP-2001.

XX

XX 08-JUL-1999; 99US-0349532.

XX

XX 09-APR-1997; 97US-0838545.

PR 09-APR-1996; 96US-0630019.

XX

XX (TEXA) UNIV TEXAS SYSTEM.

XX

XX Shay JW, Wright WE, Piatyszek MA, Corey DR, Norton JC;

XX WPI; 2001-638024/73.

XX

XX New peptide nucleic acids that hybridises to the RNA component of

PT mammalian telomerase, useful for treating or preventing cancer,

PT inflammation, lymphoproliferative diseases, autoimmune disease, or

PT neurodegenerative diseases

XX

XX Claim 7; Column 73; 46pp; English.

XX

XX The present invention relates to peptide nucleic acids (PNAs), comprising

CC a sequence of 6-25 nucleobases, that inhibit telomerase activity in

CC mammalian cells by hybridising to the RNA component of mammalian

CC telomerase. The PNAs are useful as probes to detect the RNA component

CC of mammalian telomerase and as inhibitors of telomerase activity, or to

CC detect and/or quantitate polynucleotide having the human telomerase

CC RNA component (hTR) sequence, as well as in forensic identification of

CC individuals, such as paternity testing or identification of criminal

CC suspects or unknown descendants based on the hTR gene RFLP pattern. The

CC PNA can be further used for treating or preventing cancer, inflammation,

CC lymphoproliferative diseases, autoimmune disease, or neurodegenerative

CC diseases. The PNAs in combination with other pharmaceuticals (such as

CC antineoplastic or cytostatic agents) can be used for treating neoplasia,

CC hyperplasia, human immunodeficiency virus (HIV) infections, acquired

CC immunodeficiency syndrome (AIDS) and associated pathologies, and other

CC diseases characterised by abnormal telomere metabolism or telomerase

CC activity. The present sequence represents one of the PNA sequences

CC of the invention.

XX

XX Sequence 8 BP; 1 A; 0 C; 4 G; 3 T; 0 other;

SQ

Query Match 100.0%; Score 6; DB 23; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.7e+08; Indels 0; Gaps 0;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTAA 6

Db 7 CCTAA 2

RESULT 13

AAS15474/c

ID AAS15474 standard; DNA; 8 BP.

XX

XX AAS15474;

AC

XX

DT 14-FEB-2002 (first entry)

XX

XX PNA 34 inhibiting human and mammalian telomerase activity.

DE

XX Mammalian; peptide nucleic acid; probe; forensic; paternity testing;

XX human telomerase RNA component; hTR gene RFLP pattern; cancer;

KW inflammation; lymphoproliferative disease; autoimmune disease;

KW neurodegenerative disease; neoplasia; hyperplasia; HIV; AIDS;

KW human immunodeficiency virus; acquired immunodeficiency syndrome;

KW telomere metabolism; mutant; cytostatic; anti-inflammatory;

XX immunosuppressive; polyamide backbone; ss.

OS Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

PH modified_base 1..8

FT /*tag= a

FT /note= "This sequence is a peptide nucleic acid, i.e. it

FT contains a polyamide backbone instead of a

FT deoxyribose backbone"

XX

XX modified_base 1

FT /*tag= b

FT /note= "N= 1-50 peptide nucleic acid nucleobases,

FT selected from U, T, A, G, C or i"

FT

XX modified_base 8

FT /*tag= C

FT /note= "N= 1-50 peptide nucleic acid nucleobases,

FT selected from U, T, A, G, C or i"

FT

XX US6294650-B1.

PN 25-SEP-2001.

PD

XX 08-JUL-1999; 99US-0349532.

XX

XX 09-APR-1997; 97US-0838545.

PR 09-APR-1996; 96US-0630019.

XX

XX (TEXA) UNIV TEXAS SYSTEM.

XX

XX Shay JW, Wright WE, Piatyszek MA, Corey DR, Norton JC;

XX WPI; 2001-638024/73.

XX

XX New peptide nucleic acids that hybridises to the RNA component of

PT mammalian telomerase, useful for treating or preventing cancer,

PT inflammation, lymphoproliferative diseases, autoimmune disease, or

PT neurodegenerative diseases

XX

XX Disclosure; Column 59; 46pp; English.

XX

XX The present invention relates to peptide nucleic acids (PNAs), comprising

CC a sequence of 6-25 nucleobases, that inhibit telomerase activity in

CC mammalian cells by hybridising to the RNA component of mammalian

CC telomerase. The PNAs are useful as probes to detect the RNA component

CC of mammalian telomerase and as inhibitors of telomerase activity, or to

CC detect and/or quantitate polynucleotide having the human telomerase

CC RNA component (hTR) sequence, as well as in forensic identification of

CC individuals, such as paternity testing or identification of criminal

CC suspects or unknown descendants based on the hTR gene RFLP pattern. The

CC PNA can be further used for treating or preventing cancer, inflammation,

CC lymphoproliferative diseases, autoimmune disease, or neurodegenerative

CC diseases. The PNAs in combination with other pharmaceuticals (such as

CC antineoplastic or cytostatic agents) can be used for treating neoplasia,

CC hyperplasia, human immunodeficiency virus (HIV) infections, acquired

CC immunodeficiency syndrome (AIDS) and associated pathologies, and other

CC diseases characterised by abnormal telomere metabolism or telomerase

CC activity. The present sequence represents one of the PNA sequences

CC of the invention.

XX

XX Note: The present sequence is given in the SEQ ID listing but is not

CC mentioned elsewhere in the patent.

XX

XX Sequence 8 BP; 1 A; 0 C; 3 G; 2 T; 2 other;

SQ

Query Match 100.0%; Score 6; DB 23; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.7e+08; Indels 0; Gaps 0;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

telomerase activity. Telomerase is a ribonucleoprotein enzyme that synthesizes one strand of the telomeric DNA, using as a template an 11 nucleotide sequence contained within the RNA component of the enzyme. The invention relates to PNA molecules having a sequence of no more than 25 bases, which include the sequence GTTAGG. The uncharged nature of the PNA backbone increases the melting temperature of associating strands, increases the rate of association with targeted nucleic acids, and affords greater resistance of degradation by proteases or nucleases. The therapeutic PNAs may be used for treating disease conditions such as cancers, neoplasia, hyperplasia, neurodegenerative diseases, aging, human immunodeficiency virus (HIV) infection/AIDS (acquired immunodeficiency syndrome) and associated pathologies, fungal infections, and other diseases characterized by abnormal telomere metabolism or telomerase activity, in combination with antineoplastic and other cytotoxic or cytostatic agents, antifungal agents, and other nucleotides. PNAs may be used for molecular diagnostics, labelled PNAs are used as hybridization probes to detect or quantitate polynucleotides having a human telomerase RNA (hTR) sequence. PNA probes are also used for forensic identification of individuals, e.g. paternity testing, based on hTR gene restriction fragment length polymorphism (RFLP) pattern. PNAs are also useful as probes to detect the RNA component of a mammalian telomerase and as inhibitors of telomerase activity. The method of the present invention allows cancerous conditions to be detected with increased confidence and possibly at an earlier stage, before cells are detected as cancerous based on pathological characteristics. The diagnostic and prognostic methods of the present invention can be used to detect an immortal or neoplastic cell or tumour tissue or cancer of any origin, provided the cell expresses telomerase activity and its RNA component.

Sequence 8 BP; 1 A; 0 C; 4 G; 3 T; 0 other;

Query Match 100.0%; Score 6; DB 21; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.7e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTAA 6
|||||
Db 7 CCCTAA 2

RESULT 11

AAA37572 AAA37572 standard; DNA; 8 BP.

XX AC AAA37572;

DT 15-AUG-2000 (first entry)

DE PNA sequence #30 used to inhibit telomerase activity.

XX Peptide nucleic acid; PNA; telomerase; ribonucleoprotein enzyme; cancer;
KW inhibitor; neoplasia; neurodegenerative disease; aging; hyperplasia;
KW AIDS; HIV; fungal infection; forensic identification; detect; tumour;
XX paternity testing; ss.

OS Synthetic.

XX Key Location/Qualifiers

FT misc_feature 1..8

FT /tag=

FT /note= "Peptide nucleic acid molecule, where

FT N-(2-aminoethyl)glycine units are linked to
FT nucleotide bases via glycine amino N through a
FT methylenecarbonyl linker"

XX US6046307-A.

PN 04-APR-2000.

XX 09-APR-1997; 97US-0838545.

XX 09-APR-1996; 96US-0630019.

XX

(TEXA) UNIV TEXAS SYSTEM.

XX Wright WE, Piatyszek MA, Shay JW, Norton JC, Corey DR;

XX WPI; 2000-292432/25.

XX New peptide nucleic acid (PNA) compounds that inhibit telomerase
PT activity in mammalian cells is useful as probes to detect the RNA
PT component of a mammalian telomerase

Example 2; Column 33; 45pp; English.

The present sequence represents a peptide nucleic acid molecule which hybridizes to the mRNA component of mammalian telomerase, and inhibits telomerase activity. Telomerase is a ribonucleoprotein enzyme that synthesizes one strand of the telomeric DNA, using as a template an 11 nucleotide sequence contained within the RNA component of the enzyme. The invention relates to PNA molecules having a sequence of no more than 25 bases, which include the sequence GTTAGG. The uncharged nature of the PNA backbone increases the melting temperature of associating strands, increases the rate of association with targeted nucleic acids, and affords greater resistance of degradation by proteases or nucleases. The therapeutic PNAs may be used for treating disease conditions such as cancers, neoplasia, hyperplasia, neurodegenerative diseases, aging, human immunodeficiency virus (HIV) infection/AIDS (acquired immunodeficiency syndrome) and associated pathologies, fungal infections, and other diseases characterized by abnormal telomere metabolism or telomerase activity, in combination with antineoplastic and other cytotoxic or cytostatic agents, antifungal agents, and other nucleotides. PNAs may be used for molecular diagnostics, labelled PNAs are used as hybridization probes to detect or quantitate polynucleotides having a human telomerase RNA (hTR) sequence. PNA probes are also used for forensic identification of individuals, e.g. paternity testing, based on hTR gene restriction fragment length polymorphism (RFLP) pattern. PNAs are also useful as probes to detect the RNA component of a mammalian telomerase and as inhibitors of telomerase activity. The method of the present invention allows cancerous conditions to be detected with increased confidence and possibly at an earlier stage, before cells are detected as cancerous based on pathological characteristics. The diagnostic and prognostic methods of the present invention can be used to detect an immortal or neoplastic cell or tumour tissue or cancer of any origin, provided the cell expresses telomerase activity and its RNA component.

Sequence 8 BP; 3 A; 4 C; 0 G; 1 T; 0 other;

Query Match 100.0%; Score 6; DB 21; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.7e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTAA 6
|||||
Db 2 CCCTAA 7

RESULT 12

AA515436/c

ID AA515436 standard; DNA; 8 BP.

XX AC AA515436;

DT 14-FEB-2002 (first entry)

DE PNA 28 inhibiting human and mammalian telomerase activity.

XX Mammalian; peptide nucleic acid; probe; forensic; paternity testing;
KW human telomerase RNA component; hTR gene RFLP pattern; cancer;
KW inflammation; lymphoproliferative disease; autoimmune disease;
KW neurodegenerative disease; neoplasia; hyperplasia; HIV; AIDS;
KW human immunodeficiency virus; acquired immunodeficiency syndrome;
KW telomere metabolism; mutant; cytostatic; anti-inflammatory;
KW immunosuppressive; polyamide backbone; ss.

XX Homo sapiens.

XX Oligomer hybridisable to HIV sequence and contg. peptide nucleic
 PT acid sub:unit - binds in complementary manner to DNA and RNA, and
 PT useful for modulating HIV viral activity, e.g. in treating AIDS
 XX
 PS Claim 2; Page 176; 186pp; English.
 XX
 CC New peptide nucleic acid (PNA) oligomers are provided which (a) consist
 CC of naturally occurring nucleobases covalently bound to a polyamide
 CC backbone and (b) hybridise to the translation initiation AUG region,
 CC 5' untranslated region (5' UTR), 3' untranslated region (3' UTR),
 CC splice junctions or coding sequence of a human immunodeficiency virus
 CC gene chosen from env, gag, pol, rev and tat.
 CC The PNAs can be used to target RNA and single stranded DNA (ssDNA) to
 CC produce antisense-type gene regulation moieties. They have utility
 CC as gene-targeted drugs for modulating HIV processes. Hence they
 CC can be used to treat AIDS and other viral infections. They are also
 CC useful in diagnostic applications and as research tools.
 CC PNA oligomers have high affinity for complementary single stranded DNA.
 CC They are also able to form triple helices in which a first PNA strand
 CC binds with RNA or ssDNA and a second PNA strand binds with the resulting
 CC double helix or with the first PNA strand. The PNAs possess no
 CC significant charge and are water soluble, which facilitates cellular
 CC uptake. Further, since they contain amides of non-biological amino acids,
 CC they are biostable and resistant to enzymatic degradation by proteases.
 CC The present sequence is a specifically claimed PNA sequence
 CC (represented by the sequence of nucleobases) targetting HIV genes.
 XX
 SQ Sequence 8 BP; 1 A; 0 C; 3 G; 4 T; 0 other;

Query Match 100.0%; Score 6; DB 16; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.7e+08;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTAA 6
 Db 6 CCCTAA 1

RESULT 9
 AAT89239/c
 ID AAT89239 standard; DNA; 8 BP.
 AC AAT89239;
 XX
 XX 12-MAY-1998 (first entry)
 DT
 XX
 DE Peptide nucleic acid 14, targeted to mammalian telomerase.
 XX
 XX Peptide nucleic acid; PNA; cancer; telomerase; probe; hybridisation;
 KW inhibitor; ss.
 KW
 XX Synthetic.
 OS
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..8
 FT /*tag= a
 FT /note= "Sugar-phosphate backbone has been replaced by
 FT a peptide backbone"
 XX
 PN W09738013-A1.
 XX
 PD 16-OCT-1997.
 XX
 XX 09-APR-1997; 97WO-US05931.
 XX
 XX 09-APR-1996; 96US-0630019.
 PR
 XX (GERO-) GERON CORP.
 PA
 XX Corey D, Norton JC, Piatyszek MA, Shay JW, Wright WE;
 PI
 XX WPI; 1997-512647/47.
 DR

XX New peptide nucleic acids hybridising to mammalian telomerase RNA -
 PT used to inhibit telomerase, for treating tumours and other
 PT proliferative diseases, also for diagnosis
 XX
 PS Claim 9; Page 59; 76pp; English.
 XX
 CC This sequence is a novel peptide nucleic acid (PNA), which acts as
 CC an inhibitor of mammalian, preferably human, telomerase. The PNAs
 CC hybridise specifically to an RNA component of mammalian telomerase,
 CC and include the sequence GGG for specific hybridisation to the template
 CC region of this component. PNAs can be used as probes to detect the
 CC RNA component of mammalian telomerase and as inhibitors of telomerase
 CC activity, especially in the treatment of cancer.
 XX
 SQ Sequence 8 BP; 1 A; 0 C; 4 G; 3 T; 0 other;
 Query Match 100.0%; Score 6; DB 18; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.7e+08;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCCTAA 6
 Db 7 CCCTAA 2
 RESULT 10
 AAA37558/c
 ID AAA37558 standard; DNA; 8 BP.
 XX
 AC AAA37558;
 XX
 XX 15-AUG-2000 (first entry)
 DT
 XX
 DE PNA sequence #15 used to inhibit telomerase activity.
 XX
 KW Peptide nucleic acid; PNA; telomerase; ribonucleoprotein enzyme; cancer;
 KW inhibitor; neoplasia; neurodegenerative disease; aging; hyperplasia;
 KW AIDS; HIV; fungal infection; forensic identification; detect; tumour;
 KW paternity testing; ss.
 XX
 OS .Synthetic.
 XX
 FH Key Location/Qualifiers
 FT misc_feature 1..8
 FT /*tag= a
 FT /note= "Peptide nucleic acid molecule, where
 FT N-(2-aminoethyl)glycine units are linked to
 FT nucleotide bases via glycine amino N through a
 FT methylenecarbonyl linker"
 XX
 PN US6046307-A.
 XX
 PD 04-APR-2000.
 XX
 XX 09-APR-1997; 97US-0838545.
 XX
 XX 09-APR-1996; 96US-0630019.
 PR
 XX (TEXA) UNIV TEXAS SYSTEM.
 PA
 XX Wright WE, Piatyszek MA, Shay JW, Norton JC, Corey DR;
 PI
 XX WPI; 2000-292432/25.
 DR
 XX New peptide nucleic acid (PNA) compounds that inhibit telomerase
 PT activity in mammalian cells is useful as probes to detect the RNA
 PT component of a mammalian telomerase
 XX
 XX Claim 6; Column 71; 45pp; English.
 PS
 XX The present sequence represents a peptide nucleic acid molecule which
 CC hybridises to the mRNA component of mammalian telomerase, and inhibits

```

Db          6 CCCTAA 1

RESULT 6
AAN91439
ID AAN91439 standard; DNA; 7 BP.
AC
XX AAN91439;
XX
DT 22-FEB-1990 (first entry)
XX
DE Telomere of Arabidopsis thaliana.
KW Telomere; Arabidopsis thaliana; vector; artificial chromosomes;
KW tandem repeat.
XX Arabidopsis thaliana.
OS Arabidopsis thaliana.
XX WO8909219-A.
PN
XX
PD 05-OCT-1989.
XX
XX 27-FEB-1989; 89WO-US00795.
XX
PR 24-MAR-1988; 88US-0172467.
XX
PA (GEHO-) THE GENERAL HOSPITAL CORP.
XX Richards E, Ausubel FM;
XX WPI; 1989-309497/42.
DR
XX
KW Tandem repeats (1-1000) of the telomere are used in a vector for
CC expressing specific genes in plants. They provide 'artificial
CC chromosomes' which are maintained in the nucleus, so are not subjected to
CC variable expression due to integration-position effects. They allow the
CC integration of very foreign DNA without host range limitations.
CC The telomere opt. contains variant repeats of CTCATAA. The telomere is
CC pref. the pATT4 plasmid (ATCC 67577).
XX
XX Sequence 7 BP; 3 A; 3 C; 0 G; 1 T; 0 other;
SQ
Query Match 100.0%; Score 6; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 3.1e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCCTAA 6
DB 1 CCCTAA 6
AC
XX
PS Claim 28; page 50; 65pp; English.
XX
XX Tandem repeats (1-1000) of the telomere are used in a vector for
XX expressing specific genes in plants. They provide 'artificial
XX chromosomes' which are maintained in the nucleus, so are not subjected to
XX variable expression due to integration-position effects. They allow the
XX integration of very foreign DNA without host range limitations.
XX The telomere opt. contains variant repeats of CTCATAA. The telomere is
XX pref. the pATT4 plasmid (ATCC 67577).
XX
XX Sequence 7 BP; 3 A; 3 C; 0 G; 1 T; 0 other;
SQ
Query Match 100.0%; Score 6; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 3.1e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCCTAA 6
DB 1 CCCTAA 6
AC
XX
PS Variant of Arabidopsis thaliana telomere.
XX
XX Variant telomere; Arabidopsis thaliana; vector; artificial chromosomes;
XX tandem repeat.
XX Arabidopsis thaliana.
OS Arabidopsis thaliana.
XX WO8909219-A.
PN

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XX 05-OCT-1989.
XX PD
XX PF 27-FEB-1989; 89WO-US00795.
XX PR 24-MAR-1988; 88US-0172467.
XX PA (GEHO-) THE GENERAL HOSPITAL CORP.
XX PI Richards E, Ausubel FM;
XX PP WPI; 1989-309497/42.
XX PT New recombinant DNA contg. eukaryotic telomere esp. from higher plant
XX - useful as vector for specific genes and maintained in nucleus as
XX independent replicating molecule.
XX PS Claim 35; page 50; 65pp; English.
XX CC The DNA is a variant of the telomere of the pATT4 plasmid (ATCC 67577).
XX SQ Sequence 7 BP; 3 A; 3 C; 0 G; 1 T; 0 other;
Query Match 100.0%; Score 6; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 3.1e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCCTAA 6
DB 1 CCCTAA 6
AC
XX
PS Claim 28; page 50; 65pp; English.
XX
XX Tandem repeats (1-1000) of the telomere are used in a vector for
XX expressing specific genes in plants. They provide 'artificial
XX chromosomes' which are maintained in the nucleus, so are not subjected to
XX variable expression due to integration-position effects. They allow the
XX integration of very foreign DNA without host range limitations.
XX The telomere opt. contains variant repeats of CTCATAA. The telomere is
XX pref. the pATT4 plasmid (ATCC 67577).
XX
XX Sequence 7 BP; 3 A; 3 C; 0 G; 1 T; 0 other;
SQ
Query Match 100.0%; Score 6; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 3.1e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCCTAA 6
DB 1 CCCTAA 6
AC
XX
PS Variant of Arabidopsis thaliana telomere.
XX
XX Variant telomere; Arabidopsis thaliana; vector; artificial chromosomes;
XX tandem repeat.
XX Arabidopsis thaliana.
OS Arabidopsis thaliana.
XX WO8909219-A.
PN

```

at least one (and preferably all) of the backbone subunits are composed of N-acetyl N-(2-aminoethylglycine peptide residues, the nucleobase being attached covalently to the acetyl group and the peptide linkage being formed by condensation of the glycine carboxy group of one residue with the amino group of the 2-aminoethyl moiety in the next residue"

the backone subunits are composed of N-acetyl N-(2-aminoethylglycine peptide residues, the nucleobase being attached covalently to the acetyl group and the peptide linkage being formed by condensation of the glycine carboxy group of one residue with the amino group of the 2-aminoethyl moiety in the next residue"

```

XX SQ Sequence 6 BP; 1 A; 0 C; 3 G; 2 T; 0 other;
    Query Match      100.0%; Score 6; DB 23; Length 6;
    Best Local Similarity 100.0%; Pred. No. 3.6e+08;
    Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTAA 6
    |||||
Db 6 CCCTAA 1

RESULT 4
AAS14916
ID AAS14916 standard; DNA; 6 BP.
XX AC AAS14916;
XX DT 14-FEB-2002 (first entry)
XX DE Melanogenesis associated oligonucleotide #12.
XX KW Melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53;
XX KW anti-inflammatory; dermatological; ophthalmological; anti-psoriatic;
XX KW immunosuppressive; DNA repair; proliferation inhibitor; apoptosis;
XX KW tumour necrosis factor inhibitor; photoaging; hyperproliferative disease;
XX KW carcinoma; oxidative stress; skin cancer; allergy mediated inflammation;
XX KW conjunctivitis; allergic rhinitis; vitiligo; ss.
XX OS Synthetic.
XX PN WO200174342-A2.
XX PD 11-OCT-2001.
XX PF 30-MAR-2001; 2001WO-US10162.
XX PR 31-MAR-2000; 2000US-0540843.
XX PA (UYBO-) UNIV BOSTON.
XX PI Gilchrist BA, Year M, Eller M;
XX WPI; 2001-626338/72.

Inhibiting proliferation of epithelial cells, useful e.g. for treating
carcinoma, using specific oligonucleotides that mimic the effects of
ultra-violet light -
Claim 1; Page 37; 74pp; English.

CC The invention describes inhibition of mammalian epithelial cell
CC proliferation by treating cells with at least one oligonucleotide, or
CC its fragment. The compounds, which have cytostatic, anti-allergic,
CC anti-inflammatory, dermatological, ophthalmological, anti-psoriatic and
CC immunosuppressive activities, function as 'ultra-violet mimics' to induce
CC DNA repair processes (or a protective response to later exposure to
CC radiation or chemicals) as a proliferation inhibitor, apoptosis inducer
CC or a tumour necrosis factor inhibitor. Probably they mimic products of
CC DNA damage, or processed DNA-damage intermediates, by inducing the p53
CC pathway, resulting in transient arrest of cell growth, allowing more time
CC for DNA repair to occur before cell division takes place. The method is
CC especially used to treat carcinoma but may also be used to: treat other
CC hyperproliferative states (e.g. psoriasis or precancerous conditions);
CC reduce photoaging, oxidative stress or damage; prevent skin cancer; treat
CC allergically mediated inflammation (atopic or contact dermatitis,
CC allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in
CC cells caused by radiation or chemicals; increase melanin production
CC (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to
CC promote apoptosis in epithelial cells that contain damaged DNA. Also
CC oligonucleotides that contain non-hydrolyzable backbones are used to
CC inhibit apoptosis, in response to DNA damage, in epithelial cell. This
CC sequence is melanogenesis associated oligonucleotide #12, the reverse

```

```

CC complementary sequence of AAS149015, a truncated version of the sequence
CC representing the telomere overhang sequence (AAS14909), described in the
CC method of the invention.
XX SQ Sequence 6 BP; 2 A; 3 C; 0 G; 1 T; 0 other;
    Query Match      100.0%; Score 6; DB 23; Length 6;
    Best Local Similarity 100.0%; Pred. No. 3.6e+08;
    Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTAA 6
    |||||
Db 1 CCCTAA 6

RESULT 5
ABN73654/c
ID ABN73654 standard; cDNA; 6 BP.
XX AC ABN73654;
XX DT 03-JUL-2002 (first entry)
XX DE Bovine embryonic germ (EG) cell cDNA EST 990913a CONTIG 1.
XX KW Bovine; Bos taurus; EST; expressed sequence tag; totipotence;
XX KW development; gene; ss.
XX OS Bos taurus.
XX PN WO200194550-A2.
XX PD 13-DEC-2001.
XX PF 07-JUN-2001; 2001WO-US18576.
XX PR 07-JUN-2000; 2000US-209874P.
XX PR 06-JUN-2001; 2001US-0876143.
XX PA (INFI-) INFGEN INC.
XX PI Ellertsen KJ, Pfister-Genskow M, Childs L;
XX WPI; 2002-351289/38.

An expressed sequence tag (EST), the expression of which, or its
complementary sequence, in a cell identifies the cell as a
developmentally competent or incompetent cell -
Example 16; Page 210; 584pp; English.

CC The present invention describes an expressed sequence tag (EST), where
CC the EST is an isolated, enriched, or purified nucleic acid sequence
CC representing all or part of a gene, the expression of which, or its
CC complementary sequence, in a cell identifies the cell as a
CC developmentally competent or incompetent cell. Molecules which induce
CC developmental competence in a cell line are useful for inducing
CC totipotence in one or more cells. Molecules which induce developmental
CC incompetence in a cell line are useful for preventing a full term
CC pregnancy in an animal and inhibiting totipotence. The molecules are
CC also useful for treating a disease in an animal by inducing development
CC of one or more cells of the animal into a specific cell type. The
CC present sequence represents a bovine EST which is given in the
CC exemplification of the present invention.
XX SQ Sequence 6 BP; 1 A; 0 C; 3 G; 2 T; 0 other;
    Query Match      100.0%; Score 6; DB 24; Length 6;
    Best Local Similarity 100.0%; Pred. No. 3.6e+08;
    Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTAA 6
    |||||

```

PT capacity and therefore delay cellular senescence, useful in cell
PT therapy and transplantation
XX
XX
XX Claim 12; Page 29; 38pp; English.
XX
XX Oligonucleotides AAT05734-7 are examples of telomerase substrates used
CC to increase the proliferative capacity of normal cells that express
CC telomerase activity. The oligonucleotides allow an increase in
CC length of telomeres in normal cells and in hybrids of normal and
CC immortalised cells. The increase in telomere length extends the
CC capacity of cells to replicate, esp. those treated ex vivo and used
CC for transplantation techniques e.g. cell therapy, for the treatment
CC of AIDS, anaemia, leukaemia or lymphoma.
XX
XX Sequence 6 BP; 1 A; 0 C; 3 G; 2 T; 0 other;
SQ

Query Match 100.0%; Score 6; DB 16; Length 6;
Best Local Similarity 100.0%; Pred. No. 3.6e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX

QY 1 CCCTAA 6
Db 6 CCCTAA 1
|||||

RESULT 2
AAS14915/c
ID AAS14915 standard; DNA; 6 BP.
XX
XX AAS14915;
XX
XX 14-FEB-2002 (first entry)
XX
XX Melanogenesis associated oligonucleotide #11.
XX
XX Melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53;
KW anti-inflammatory; dermatological; ophthalmological; anti-psoriatic;
KW immunosuppressive; DNA repair; proliferation inhibitor; apoptosis;
KW tumour necrosis factor inhibitor; photoaging; hyperproliferative disease;
KW carcinoma; oxidative stress; skin cancer; allergy mediated inflammation;
KW conjunctivitis; allergic rhinitis; vitiligo; ss.
XX
XX Synthetic.
XX
XX WO200174342-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US10162.
XX
XX 31-MAR-2000; 2000US-0540843.
XX
XX (UYBO-) UNIV BOSTON.
XX
XX Gilchrist BA, Yaar M, Eller M;
XX WPI; 2001-626338/72.
XX
XX Inhibiting proliferation of epithelial cells, useful e.g. for treating
PT carcinoma, using specific oligonucleotides that mimic the effects of
PT ultra-violet light -
XX
XX Claim 1; Page 37; 74pp; English.
XX
XX The invention describes inhibition of mammalian epithelial cell
CC proliferation by treating cells with at least one oligonucleotide, or
CC its fragment. The compounds, which have cytostatic, anti-allergic,
CC anti-inflammatory, dermatological, ophthalmological, anti-psoriatic and
CC immunosuppressive activities, function as 'ultra-violet mimics' to induce
CC DNA repair processes (or a protective response to later exposure to
CC radiation or chemicals), as a proliferation inhibitor, apoptosis inducer
CC or a tumour necrosis factor inhibitor. Probably they mimic products of
CC DNA damage, or processed DNA-damage intermediates, by inducing the p53
CC pathway, resulting in transient arrest of cell growth, allowing more time
CC for DNA repair to occur before cell division takes place. The method is
CC especially used to treat carcinoma but may also be used to: treat other
CC hyperproliferative states (e.g. psoriasis or precancerous conditions);
CC reduce photoaging, oxidative stress or damage; prevent skin cancer; treat
CC allergically mediated inflammation (atopic or contact dermatitis,
CC allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in
CC cells caused by radiation or chemicals; increase melanin production
CC (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to
CC promote apoptosis in epithelial cells that contain damaged DNA. Also
CC oligonucleotides that contain non-hydrolyzable backbones are used to
CC inhibit apoptosis, in response to DNA damage, in epithelial cell. This
CC sequence is melanogenesis associated oligonucleotide #11, a truncated
CC version of the sequence representing the telomere overhang sequence
CC (AAS14909) and one of the oligonucleotides used to inhibit mammalian
XX epithelial cell proliferation, described in the method of the invention.

PT capacity and therefore delay cellular senescence, useful in cell
PT therapy and transplantation
XX
XX
XX Claim 12; Page 29; 38pp; English.
XX
XX Oligonucleotides AAT05734-7 are examples of telomerase substrates used
CC to increase the proliferative capacity of normal cells that express
CC telomerase activity. The oligonucleotides allow an increase in
CC length of telomeres in normal cells and in hybrids of normal and
CC immortalised cells. The increase in telomere length extends the
CC capacity of cells to replicate, esp. those treated ex vivo and used
CC for transplantation techniques e.g. cell therapy, for the treatment
CC of AIDS, anaemia, leukaemia or lymphoma.
XX
XX Sequence 6 BP; 1 A; 0 C; 3 G; 2 T; 0 other;
SQ

Query Match 100.0%; Score 6; DB 20; Length 6;
Best Local Similarity 100.0%; Pred. No. 3.6e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX

QY 1 CCCTAA 6
Db 6 CCCTAA 1
|||||

RESULT 3
AAS14915/c
ID AAS14915 standard; DNA; 6 BP.
XX
XX AAS14915;
XX
XX 14-FEB-2002 (first entry)
XX
XX Melanogenesis associated oligonucleotide #11.
XX
XX Melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53;
KW anti-inflammatory; dermatological; ophthalmological; anti-psoriatic;
KW immunosuppressive; DNA repair; proliferation inhibitor; apoptosis;
KW tumour necrosis factor inhibitor; photoaging; hyperproliferative disease;
KW carcinoma; oxidative stress; skin cancer; allergy mediated inflammation;
KW conjunctivitis; allergic rhinitis; vitiligo; ss.
XX
XX Synthetic.
XX
XX WO200174342-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US10162.
XX
XX 31-MAR-2000; 2000US-0540843.
XX
XX (UYBO-) UNIV BOSTON.
XX
XX Gilchrist BA, Yaar M, Eller M;
XX WPI; 2001-626338/72.
XX
XX Inhibiting proliferation of epithelial cells, useful e.g. for treating
PT carcinoma, using specific oligonucleotides that mimic the effects of
PT ultra-violet light -
XX
XX Claim 1; Page 37; 74pp; English.
XX
XX The invention describes inhibition of mammalian epithelial cell
CC proliferation by treating cells with at least one oligonucleotide, or
CC its fragment. The compounds, which have cytostatic, anti-allergic,
CC anti-inflammatory, dermatological, ophthalmological, anti-psoriatic and
CC immunosuppressive activities, function as 'ultra-violet mimics' to induce
CC DNA repair processes (or a protective response to later exposure to
CC radiation or chemicals), as a proliferation inhibitor, apoptosis inducer
CC or a tumour necrosis factor inhibitor. Probably they mimic products of
CC DNA damage, or processed DNA-damage intermediates, by inducing the p53
CC pathway, resulting in transient arrest of cell growth, allowing more time
CC for DNA repair to occur before cell division takes place. The method is
CC especially used to treat carcinoma but may also be used to: treat other
CC hyperproliferative states (e.g. psoriasis or precancerous conditions);
CC reduce photoaging, oxidative stress or damage; prevent skin cancer; treat
CC allergically mediated inflammation (atopic or contact dermatitis,
CC allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in
CC cells caused by radiation or chemicals; increase melanin production
CC (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to
CC promote apoptosis in epithelial cells that contain damaged DNA. Also
CC oligonucleotides that contain non-hydrolyzable backbones are used to
CC inhibit apoptosis, in response to DNA damage, in epithelial cell. This
CC sequence is melanogenesis associated oligonucleotide #11, a truncated
CC version of the sequence representing the telomere overhang sequence
CC (AAS14909) and one of the oligonucleotides used to inhibit mammalian
XX epithelial cell proliferation, described in the method of the invention.

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 6, 2003, 06:40:37 ; Search time 132.857 seconds
(without alignments)
101.703 Million cell updates/sec

Title: US-09-540-843-12

Perfect score: 6

Sequence: 1 ccctaa 6

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 2063506

Minimum DB seq length: 0

Maximum DB seq length: 40

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_101002.*

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19: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.*
20: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.*
21: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	6	100.0	6	AA05734	Telomerase oligonu
C 2	6	100.0	6	AA05734	Telomeric repeat s
C 3	6	100.0	6	AA05734	Melanogenesis asso
C 4	6	100.0	6	AA05734	Melanogenesis asso
C 5	6	100.0	6	AA05734	Bovine embryonic g
C 6	6	100.0	7	AA05734	Telomere of Arabid
C 7	6	100.0	7	AA05734	Variant of Arabido
C 8	6	100.0	8	AA05734	Peptide nucleic ac
C 9	6	100.0	8	AA05734	Peptide nucleic ac

C 10	6	100.0	8	21	AAA37558	PNA sequence #15 u
C 11	6	100.0	8	21	AAA37572	PNA sequence #30 u
C 12	6	100.0	8	23	AA05734	PNA 28 inhibiting
C 13	6	100.0	8	23	AA05734	PNA 34 inhibiting
C 14	6	100.0	9	16	AA05735	Telomerase oligonu
C 15	6	100.0	9	18	AA05735	Peptide nucleic ac
C 16	6	100.0	9	18	AA05735	Telomerase substra
C 17	6	100.0	9	20	AA05735	Telomere motif mim
C 18	6	100.0	9	21	AA05755	PNA sequence #16 u
C 19	6	100.0	9	21	AA05755	Primer for human t
C 20	6	100.0	9	22	AA05755	Human breast cance
C 21	6	100.0	9	23	AA05755	PNA 29 inhibiting
C 22	6	100.0	9	24	AA05755	Drosophila bicoid
C 23	6	100.0	10	18	AA05755	N3 to P5 oligonuc
C 24	6	100.0	10	18	AA05755	N3 to P5 oligonuc
C 25	6	100.0	10	18	AA05755	Peptide nucleic ac
C 26	6	100.0	10	18	AA05755	DNA oligonucleotid
C 27	6	100.0	10	18	AA05755	Peptide nucleic ac
C 28	6	100.0	10	19	AA05755	Antisense oligonuc
C 29	6	100.0	10	20	AA05755	Lung cancer indica
C 30	6	100.0	10	20	AA05755	Random amplified p
C 31	6	100.0	10	20	AA05755	Telomere motif mim
C 32	6	100.0	10	20	AA05755	Telomere motif mim
C 33	6	100.0	10	21	AA05755	Human macrophage g
C 34	6	100.0	10	21	AA05755	PNA sequence #7 us
C 35	6	100.0	10	21	AA05755	Template region of
C 36	6	100.0	10	21	AA05755	PNA sequence #17 u
C 37	6	100.0	10	21	AA05755	PNA sequence #21 u
C 38	6	100.0	10	21	AA05755	PNA sequence #29 u
C 39	6	100.0	10	21	AA05755	Human dendritic ce
C 40	6	100.0	10	21	AA05755	Human dendritic ce
C 41	6	100.0	10	21	AA05755	Human dendritic ce
C 42	6	100.0	10	21	AA05755	Human dendritic ce
C 43	6	100.0	10	21	AA05755	Metastatic breast
C 44	6	100.0	10	21	AA05755	Metastatic breast
C 45	6	100.0	10	21	AA05755	Metastatic breast

ALIGNMENTS

RESULT 1
AA05734/c
ID AA05734 standard; DNA; 6 BP.
XX
AC AA05734;
XX
DT 01-FEB-1996 (first entry)
XX
DE Telomerase oligonucleotide substrate #1.

XX Telomerase; proliferation; telomere; hybrid; immortalised cell; anaemia;
XX transplacental; cell therapy; treatment; AIDS; leukaemia; lymphoma; ss.

OS Synthetic.

XX WO9513383-A1.

PN 18-MAY-1995.

PD 10-NOV-1994; 94WO-US13130.

PF 12-NOV-1993; 93US-0153051.

PR 12-NOV-1993; 93US-0151477.

XX (GERO-) GERON CORP.

XX (TEXA) UNIV TEXAS SYSTEM.

XX Shay J, West MD, Wright WE;

XX WPI; 1995-224051/29.

XX Increasing telomere length in cells - to increase proliferative

PT

REFERENCE AUTHORS TITLE JOURNAL COMMENT

1 (bases 1 to 21)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Other_ESRs: 2821108.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
Scores: PHRED from University of Washington Genome Center
Trimming: cross_match from University of Washington Genome Center
PRAP suite, Poly-T Identification: patMatch.pl from Berkeley
Drosophila Genome Project, University of Washington Genome Center:
<http://www.genome.washington.edu> Low Quality sequence: 10
contiguous PHRED high quality bases following vector sequence. Very
Low Quality Sequence: Trace file contained 21 contiguous distinct
peaks following vector sequence. Polyadenylation: Based upon the
presence of a XhoI site followed by a run of 14 or more T residues
at the beginning of the sequence, this cDNA insert was
polyadenylated.
Plate: LLCM5 row: P column: 5
High quality sequence stop: 10.
Location/Qualifiers

FEATURES source

1. .21
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2821108"
/clone_lib="NIH_MGC_7"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCAGGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 4 a 6 c 0 g 11 t
ORIGIN
Query Match 100.0%; Score 6; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTAA 6
|||||
Db 15 CCCTAA 20

RESULT 15 A2331625 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

A2331625 21 bp DNA linear GSS 29-SEP-2000
LM0059M07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0059M07 R, DNA sequence.
A2331625
A2331625.1 GI:10394498
GSS.
house mouse.
Mus musculus

REFERENCE AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb

TITLE

JOURNAL COMMENT

plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dduun@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0059 row: M column: 07
Seq primer: CACACAGGAACACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0059M07"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: pWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT ORIGIN

Query Match 100.0%; Score 6; DB 17; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTAA 6
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Db 11 CCCTAA 16

Search completed: July 6, 2003, 09:39:51
Job time : 894.643 secs

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/organism="Trypanosoma brucei"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="158a03"

BASE COUNT      6 a      11 c      0 g      3 t
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Query Match      100.0%; Score 6; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCCTAA 6
        |||||
Db      2 CCCTAA 7

RESULT 12
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LOCUS      20 bp      DNA      linear      GSS 13-DEC-2000
DEFINITION      T. brucei sheared genomic DNA clone 199g02, reverse sequence,
genomic survey sequence.
ACCESSION      AL476798
VERSION      AL476798.1 GI:11843362
KEYWORDS
SOURCE      Trypanosoma brucei.
ORGANISM      Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
REFERENCE
AUTHORS      Hall, N., Bowman, S., Lennard, N. J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S. E., Rajadream, M. A. and Barrell, B. G.
TITLE      Direct Submission
JOURNAL
COMMENT      Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nhs@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 Gutat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J. C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES
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Location/Qualifiers
/organism="Trypanosoma brucei"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="199g02"

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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 4.5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCCTAA 6
        |||||
Db      15 CCCTAA 20

RESULT 13
AW248826
LOCUS      21 bp      mRNA      linear      EST 07-JAN-2000
DEFINITION      2821056.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821056 3',
mRNA sequence.
ACCESSION      AW248826

/organism="Trypanosoma brucei"
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/db_xref="taxon:5691"
/clone="158a03"

BASE COUNT      6 a      11 c      0 g      3 t
ORIGIN

Query Match      100.0%; Score 6; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCCTAA 6
        |||||
Db      15 CCCTAA 20

RESULT 14
AW248836
LOCUS      21 bp      mRNA      linear      EST 07-JAN-2000
DEFINITION      2821108.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821108 3',
mRNA sequence.
ACCESSION      AW248836
VERSION      AW248836.1 GI:6591829
KEYWORDS
SOURCE      Homo sapiens
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

/organism="Trypanosoma brucei"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="158a03"

BASE COUNT      6 a      11 c      0 g      3 t
ORIGIN

Query Match      100.0%; Score 6; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCCTAA 6
        |||||
Db      15 CCCTAA 20

RESULT 14
AW248836
LOCUS      21 bp      mRNA      linear      EST 07-JAN-2000
DEFINITION      2821108.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821108 3',
mRNA sequence.
ACCESSION      AW248836
VERSION      AW248836.1 GI:6591829
KEYWORDS
SOURCE      Homo sapiens
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0071D09"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT      2 a      2 c      10 g      6 t
ORIGIN

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Query Match 100.0%; Score 6; DB 17; Length 20;
 Best Local Similarity 100.0%; Pred. No. 4.5e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 CCCTAA 6
    |||||
Db 11 CCCTAA 6

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RESULT 10
AZ960008
LOCUS      20 bp      DNA      linear      GSS 27-APR-2001
DEFINITION 2M0227G31R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0227G31 R, DNA sequence.
ACCESSION  AZ960008
VERSION     AZ960008.1 GI:13831235
KEYWORDS   GSS.
SOURCE     house mouse.
ORGANISM   Mus musculus
REFERENCE  1 (bases 1 to 20)
AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL   Unpublished (2000)
COMMENT   Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0227 row: G column: 21
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
FEATURES   Location/Qualifiers
            source
              1..20

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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0227G21"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, Tl-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT      8 a      5 c      2 g      5 t
ORIGIN

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Query Match 100.0%; Score 6; DB 17; Length 20;
 Best Local Similarity 100.0%; Pred. No. 4.5e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 CCCTAA 6
    |||||
Db 13 CCCTAA 18

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RESULT 11
TA158A03P
LOCUS      20 bp      DNA      linear      GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 158A03, forward sequence,
genomic survey sequence.
ACCESSION  AL472050
VERSION     AL472050.1 GI:11837404
KEYWORDS   GSS.
SOURCE     Trypanosoma brucei.
ORGANISM   Trypanosoma brucei
REFERENCE  1 (bases 1 to 20)
AUTHORS   Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Meiville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE     Direct Submission
JOURNAL   Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk
COMMENT   Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES   Location/Qualifiers
            source
              1..20

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/organism="Mus musculus"
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT      5 a      7 g      6 t
ORIGIN

```

```

Query Match      100.0%; Score 6; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 CCCTAA 6
        |||||
Db      18 CCCTAA 13

```

```

RESULT 8
AZ662909/c
LOCUS      20 bp      DNA      linear      GSS 14-DEC-2000
DEFINITION 1M0542G17F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0542G17 F, DNA sequence.
ACCESSION  AZ662909
VERSION     AZ662909.1
KEYWORDS   GSS.
SOURCE     house mouse.
ORGANISM   Mus musculus

```

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0542 row: G column: 17
Seq primer: CGTTGTAAGGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.

```

```

FEATURES
source

```

```

1. .20

```

```

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0542G17"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT      2 a      2 c      11 g      5 t
ORIGIN

```

```

Query Match      100.0%; Score 6; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 CCCTAA 6
        |||||
Db      12 CCCTAA 7

```

```

RESULT 9
AZ808291/c
LOCUS      20 bp      DNA      linear      GSS 20-FEB-2001
DEFINITION 2M0071D09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0071D09 R, DNA sequence.
ACCESSION  AZ808291
VERSION     AZ808291.1
KEYWORDS   GSS.
SOURCE     house mouse.
ORGANISM   Mus musculus

```

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0071 row: D column: 09
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.

```

```

FEATURES
source

```

```

1. .20

```

```

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0102N07"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT      8 a      6 c      2 g      3 t
ORIGIN

Query Match      100.0%; Score 6; DB 17; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTAA 6
    |||||
Db 12 CCCTAA 17

RESULT 6
AZ345513      20 bp      DNA      linear      GSS 29-SEP-2000
LOCUS      1M0080J04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION      clone UUGC1M0080J04 F, DNA sequence.
ACCESSION      AZ345513
VERSION      AZ345513.1 GI:10424750
KEYWORDS      GSS.
SOURCE      house mouse.
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0080 row: J column: 04
Seq primer: CGTTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 20.
FEATURES
Location/Qualifiers
1..20
source

```

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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0080J04"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT      3 a      13 c      0 g      4 t
ORIGIN

Query Match      100.0%; Score 6; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTAA 6
    |||||
Db 11 CCCTAA 16

RESULT 7
AZ627174/c
LOCUS      1M0467010R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION      clone UUGC1M0467010 R, DNA sequence.
ACCESSION      AZ627174
VERSION      AZ627174.1 GI:11749364
KEYWORDS      GSS.
SOURCE      house mouse.
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0467 row: O column: 10
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
FEATURES
Location/Qualifiers
1..20
source

```

```

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCLM0200F10"
/clone_lib="Mouse 10kb plasmid UUGCLM library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (g114732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT      7 a      5 c      2 g      5 t
ORIGIN

```

```

Query Match      100.0%; Score 6; DB 17; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 CCCTAA 6
        |||||
DB      3 CCCTAA 8

```

```

RESULT 4
LOCUS      A2614760/c
DEFINITION 1M0443A17R Mouse 10kb plasmid UUGCLM library Mus musculus genomic
clone UUGCLM0443A17 R, DNA sequence.
ACCESSION  A2614760
VERSION     GSS.
KEYWORDS    house mouse.
SOURCE      Mus musculus

```

```

ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

```

```

TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
JOURNAL
COMMENT    Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0443 row: A column: 17
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
1. .19

```

```

FEATURES
source

```

```

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCLM0443A17"
/clone_lib="Mouse 10kb plasmid UUGCLM library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (g114732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT      3 a      0 c      10 g      6 t
ORIGIN

```

```

Query Match      100.0%; Score 6; DB 17; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 CCCTAA 6
        |||||
DB      15 CCCTAA 10

```

```

RESULT 5
LOCUS      A2826736
DEFINITION 2M0102N07R Mouse 10kb plasmid UUGCLM library Mus musculus genomic
clone UUGCLM0102N07 R, DNA sequence.
ACCESSION  A2826736
VERSION     GSS.
KEYWORDS    house mouse.
SOURCE      Mus musculus

```

```

ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

```

```

TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
JOURNAL
COMMENT    Unpublished (2000)
Contact: Robert B. Weiss
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University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0102 row: N column: 07
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
1. .19

```

```

FEATURES
source

```

http://www.genome.washington.edu Low Quality Sequence: 15
contiguous PHRED high quality bases following vector sequence. Very
Low Quality Sequence: Trace file contained 16 contiguous distinct
peaks following vector sequence. Polyadenylation: Based upon the
presence of a XhoI site followed by a run of 14 or more T residues
at the beginning of the sequence, this cDNA insert was
polyadenylated.
Plate: L10C1 row: K column: 7
High quality sequence stop: 15.
Location/Qualifiers
1. .16
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2819454"
/clone_lib="NH_MGC_7"
/tissue_type="small cell carcinoma"
/cell_line="MCC3"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

FEATURES

source

BASE COUNT 3 a 0 c 3 g 10 t
ORIGIN
Query Match 100.0%; Score 6; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.2e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTAA 6
|||||
Db 14 CCCTAA 9

RESULT 2

AZ392246/c
LOCUS 19 bp DNA linear GSS 03-OCT-2000
DEFINITION 1M0154G12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0154G12 R, DNA sequence.
ACCESSION AZ392246
VERSION AZ392246.1 GI:10507234
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0154 row: G column: 12
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES

source

Location/Qualifiers
1. .19

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0154G12"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, P-"
/note="Vector: pWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 3 a 5 c 5 g 6 t
ORIGIN

Query Match 100.0%; Score 6; DB 17; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTAA 6
|||||
Db 19 CCCTAA 14

RESULT 3

AZ422271
LOCUS 19 bp DNA linear GSS 03-OCT-2000
DEFINITION 1M0200F10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0200F10 R, DNA sequence.

ACCESSION AZ422271
VERSION AZ422271.1 GI:10546284
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0200 row: F column: 10
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES

source

Location/Qualifiers
1. .19

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 6, 2003, 07:33:45 : Search time 894.643 Seconds
(without alignments)
108.616 Million cell updates/sec

Title: US-09-540-843-12

Perfect score: 6

Sequence: 1 ccctaa 6

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 60474

Minimum DB seq length: 0

Maximum DB seq length: 40

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

```
EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pin:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	6	100.0	16	10	AW248958
C 2	6	100.0	19	17	AZ392246
C 3	6	100.0	19	17	AZ422271
C 4	6	100.0	19	17	AZ614760
C 5	6	100.0	19	17	AZ826736
C 6	6	100.0	20	17	AZ345513
C 1	6	100.0	16	10	AW248958
C 2	6	100.0	19	17	AZ392246
C 3	6	100.0	19	17	AZ422271
C 4	6	100.0	19	17	AZ614760
C 5	6	100.0	19	17	AZ826736
C 6	6	100.0	20	17	AZ345513

C 7	6	100.0	20	17	AZ627174	AZ627174	1M0467010
C 8	6	100.0	20	17	AZ662909	AZ662909	1M0542617
C 9	6	100.0	20	17	AZ808291	AZ808291	2M0071D09
C 10	6	100.0	20	17	AZ960008	AZ960008	2M0227621
C 11	6	100.0	20	17	TA158A03P	TA158A03P	AL472050 T. brucei
C 12	6	100.0	20	17	TA199C02Q	TA199C02Q	AL476798 T. brucei
C 13	6	100.0	21	10	AW248826	AW248826	2821056.3
C 14	6	100.0	21	10	AW248836	AW248836	2821108.3
C 15	6	100.0	21	17	AZ331625	AZ331625	1M0059M07
C 16	6	100.0	21	17	AZ399400	AZ399400	1M0165C13
C 17	6	100.0	21	17	AZ445481	AZ445481	1M0241P15
C 18	6	100.0	21	17	AZ626594	AZ626594	1M0466J20
C 19	6	100.0	21	17	AZ760907	AZ760907	1M0554P21
C 20	6	100.0	21	17	AZ766315	AZ766315	1M0563K14
C 21	6	100.0	21	17	AZ828389	AZ828389	2M0103P16
C 22	6	100.0	21	17	AZ833919	AZ833919	2M0116N18
C 23	6	100.0	21	17	AZ877328	AZ877328	2M0192C18
C 24	6	100.0	22	9	AA954126	AA954126	oq66a07.s
C 25	6	100.0	22	9	AA527213	AA527213	ni27b11.s
C 26	6	100.0	22	14	D18745	D18745	MUSGS01807
C 27	6	100.0	22	17	AZ324747	AZ324747	1M0046013
C 28	6	100.0	22	17	AZ464647	AZ464647	1M0274D09
C 29	6	100.0	22	17	AZ483833	AZ483833	1M0310H03
C 30	6	100.0	22	17	AZ500414	AZ500414	1M0338G17
C 31	6	100.0	22	17	AZ598320	AZ598320	1M0413N04
C 32	6	100.0	22	17	AZ629501	AZ629501	1M0482G06
C 33	6	100.0	22	17	AZ666649	AZ666649	1M0548M19
C 34	6	100.0	22	17	AZ836104	AZ836104	2M0130C17
C 35	6	100.0	22	17	AZ855118	AZ855118	2M0159H05
C 36	6	100.0	23	9	AU258772	AU258772	AU258772
C 37	6	100.0	23	17	AZ423815	AZ423815	1M0203O23
C 38	6	100.0	23	17	AZ465280	AZ465280	1M0275A10
C 39	6	100.0	23	17	AZ623979	AZ623979	1M0462E14
C 40	6	100.0	23	17	AZ817008	AZ817008	2M0086E02
C 41	6	100.0	23	17	AZ979817	AZ979817	2M0256F09
C 42	6	100.0	23	17	BH857265	BH857265	SALK_0765
C 43	6	100.0	24	17	AZ309633	AZ309633	1M0016B22
C 44	6	100.0	24	17	AZ785628	AZ785628	2M0029M09
C 45	6	100.0	24	17	AZ806300	AZ806300	2M0068F13

ALIGNMENTS

RESULT 1
AW248958/c
LOCUS 2819454.3prime NIH_MGC_7 16 bp mRNA linear EST 07-JAN-2000
DEFINITION 2819454.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819454 3', mRNA sequence.
ACCESSION AW248958
VERSION AW248958.1 GI:6591951
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 16)
AUTHORS NIH-MSC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Other_ESTs: 2819454.5prime
Contact: Robert Strausberg, Ph.D.
Email: cqabps-r@mail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
Scores: PHRED from University of Washington Genome Center. Vector
Trimming: cross_match from University of Washington Genome Center
PHRAP suite. Poly-T identification: patmatch.pl from Berkeley
Drosophila Genome Project. University of Washington Genome Center:

Search completed: July 6, 2003, 12:17:04
Job time : 65.5714 secs

Best Local Similarity 100.0%; Pred. No. 1.7e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTAA 6
Db 1 CCCTAA 6

RESULT 14

US-10-044-692-294/c
; Sequence 294, Application US/10044692
; Publication No. US200300963441

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.

Lingner, Joachim

Nakamura, Toru

Chapman, Karen B.

Morin, Gregg B.

Harley, Calvin

Andrews, William H.

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QY      1 CCCTAA 6
      111111
Db      6 CCCTAA 1

RESULT 10
US-09-730-893-6/c
; Sequence 6, Application US/09730893
; Patent No. US20020107258A1
; GENERAL INFORMATION:
; APPLICANT: KERWIN, SEAN M.
; APPLICANT: FEDOROFF, OLEG Y.
; APPLICANT: SALAZAR, MIGUEL
; APPLICANT: HURLEY, LAURENCE H.
; TITLE OF INVENTION: INHIBITION OF HUMAN TELOMERASE BY A
; FILE REFERENCE: UTSB:679USC1
; CURRENT APPLICATION NUMBER: US/09/730,893
; CURRENT FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 09/244,675
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: 60/073,629
; PRIOR FILING DATE: 1998-04-02
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 7
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-730-893-6

Query Match      100.0%; Score 6; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.2e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCCTAA 6
      111111
Db      6 CCCTAA 1

RESULT 11
US-09-940-173A-4/c
; Sequence 4, Application US/09940173A
; Publication No. US20030040525A1
; GENERAL INFORMATION:
; APPLICANT: KERWIN, SEAN M.
; APPLICANT: FEDOROFF, OLEG Y.
; APPLICANT: SALAZAR, MIGUEL
; APPLICANT: HURLEY, LAURENCE H.
; TITLE OF INVENTION: INHIBITION OF HUMAN TELOMERASE BY A
; FILE REFERENCE: UTSB:679USD2
; CURRENT APPLICATION NUMBER: US/09/940,173A
; CURRENT FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: 09/730,893
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 09/244,675
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: 60/073,629
; PRIOR FILING DATE: 1998-04-02
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 8
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

Query Match      100.0%; Score 6; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.2e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCCTAA 6
      111111
Db      6 CCCTAA 1

RESULT 12
US-09-730-893-4/c
; Sequence 4, Application US/09730893
; Patent No. US20020107258A1
; GENERAL INFORMATION:
; APPLICANT: KERWIN, SEAN M.
; APPLICANT: FEDOROFF, OLEG Y.
; APPLICANT: SALAZAR, MIGUEL
; APPLICANT: HURLEY, LAURENCE H.
; TITLE OF INVENTION: INHIBITION OF HUMAN TELOMERASE BY A
; FILE REFERENCE: UTSB:679USC1
; CURRENT APPLICATION NUMBER: US/09/730,893
; CURRENT FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 09/244,675
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: 60/073,629
; PRIOR FILING DATE: 1998-04-02
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 8
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-730-893-4

Query Match      100.0%; Score 6; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCCTAA 6
      111111
Db      6 CCCTAA 1

RESULT 13
US-09-728-574-19
; Sequence 19, Application US/09728574
; Patent No. US20020137036A1
; GENERAL INFORMATION:
; APPLICANT: STRATAGENE
; TITLE OF INVENTION: Methods for Detection of a Target Nucleic Acid By Capture
; FILE REFERENCE: 25436/1660
; CURRENT APPLICATION NUMBER: US/09/728,574
; CURRENT FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 09/728574
; PRIOR FILING DATE: 2000-11-30
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Drosophila sp.
; FEATURE:
; NAME/KEY: bicoid DNA binding site
; LOCATION: (1)..(9)
US-09-728-574-19

Query Match      100.0%; Score 6; DB 10; Length 9;
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Best Local Similarity 100.0%; Pred. No. 2.5e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTAA 6
Db 6 CCCTAA 1

RESULT 6
US-09-817-387-29/c
; Sequence 29, Application US/09817387
; Patent No. US20010039263A1
; GENERAL INFORMATION:
; APPLICANT: Max-Delbruck-Centrum fur Molekulare Medizin
; TITLE OF INVENTION: Chimeric Oligonucleotides and the Use Thereof
; FILE REFERENCE: 101195-24
; CURRENT APPLICATION NUMBER: US/09/817,387
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: DE 197 20 151.2
; PRIOR FILING DATE: 1997-05-02
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: telomeric
; OTHER INFORMATION: DNA of man
US-09-817-387-29

Query Match 100.0%; Score 6; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTAA 6
Db 6 CCCTAA 1

RESULT 7
US-09-735-363A-49/c
; Sequence 49, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
; APPLICANT: Fillion, Mario
; APPLICANT: Phillip, Nigel
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 49
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-735-363A-49

Query Match 100.0%; Score 6; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTAA 6
Db 6 CCCTAA 1

RESULT 8
US-09-730-893-1/c
; Sequence 1, Application US/09730893
; Patent No. US20020107258A1
; GENERAL INFORMATION:
; APPLICANT: KERWIN, SEAN M.
; APPLICANT: FEDOROFF, OLEG Y.
; APPLICANT: SALAZAR, MIGUEL
; APPLICANT: HURLEY, LAURENCE H.
; TITLE OF INVENTION: INHIBITION OF HUMAN TELOMERASE BY A
; FILE REFERENCE: UTSB:679USD1
; CURRENT APPLICATION NUMBER: US/09/730,893
; CURRENT FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 09/244,675
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: 60/073,629
; PRIOR FILING DATE: 1998-04-02
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-09-730-893-1

Query Match 100.0%; Score 6; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTAA 6
Db 6 CCCTAA 1

RESULT 9
US-09-940-173A-6/c
; Sequence 6, Application US/09940173A
; Publication No. US20030040525A1
; GENERAL INFORMATION:
; APPLICANT: KERWIN, SEAN M.
; APPLICANT: FEDOROFF, OLEG Y.
; APPLICANT: SALAZAR, MIGUEL
; APPLICANT: HURLEY, LAURENCE H.
; TITLE OF INVENTION: INHIBITION OF HUMAN TELOMERASE BY A
; FILE REFERENCE: UTSB:679USD2
; CURRENT APPLICATION NUMBER: US/09/940,173A
; CURRENT FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: 09/730,893
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 09/244,675
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: 60/073,629
; PRIOR FILING DATE: 1998-04-02
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 7
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-09-940-173A-6

Query Match 100.0%; Score 6; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.2e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 2
US-10-122-630-12
; Sequence 12, Application US/10122630
; Publication No. US20030032610A1
; GENERAL INFORMATION:
; APPLICANT: Gilchrest, Barbara A.
; APPLICANT: Eller, Mark S.
; APPLICANT: Yaar, Mina
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using
; FILE REFERENCE: 0054.1088-018
; CURRENT APPLICATION NUMBER: US/10/122,630
; CURRENT FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 08/467,012
; PRIOR FILING DATE: 1993-06-06
; PRIOR APPLICATION NUMBER: PCT/US96/08386
; PRIOR FILING DATE: 1996-06-03
; PRIOR APPLICATION NUMBER: US 09/048,927
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: US 09/540,843
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: PCT/US01/10162
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-630-12

Query Match 100.0%; Score 6; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTAA 6
| | | | |
Db 1 CCCTAA 6

RESULT 3
US-10-122-633-11/c
; Sequence 11, Application US/10122633
; Publication No. US20030032611A1
; GENERAL INFORMATION:
; APPLICANT: Gilchrest, Barbara A.
; APPLICANT: Eller, Mark S.
; APPLICANT: Yaar, Mina
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using
; FILE REFERENCE: 0054.1088-019
; CURRENT APPLICATION NUMBER: US/10/122,633
; CURRENT FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 09/540,843
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: PCT/US01/10162
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-633-11

Query Match 100.0%; Score 6; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTAA 6
| | | | |
Db 6 CCCTAA 1

RESULT 4
US-10-122-633-12
; Sequence 12, Application US/10122633
; Publication No. US20030032611A1
; GENERAL INFORMATION:
; APPLICANT: Gilchrest, Barbara A.
; APPLICANT: Eller, Mark S.
; APPLICANT: Yaar, Mina
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using
; FILE REFERENCE: 0054.1088-019
; CURRENT APPLICATION NUMBER: US/10/122,633
; CURRENT FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 09/540,843
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: PCT/US01/10162
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-633-12

Query Match 100.0%; Score 6; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTAA 6
| | | | |
Db 1 CCCTAA 6

RESULT 5
US-09-940-173A-1/c
; Sequence 1, Application US/09940173A
; Publication No. US20030040525A1
; GENERAL INFORMATION:
; APPLICANT: KERWIN, SEAN M.
; APPLICANT: FEDOROFF, OLEG Y.
; APPLICANT: SALAZAR, MIGUEL
; APPLICANT: HURLEY, LAURENCE H.
; TITLE OF INVENTION: INHIBITION OF HUMAN TELOMERASE BY A
; FILE REFERENCE: UTSB:679USD2
; CURRENT APPLICATION NUMBER: US/09/940,173A
; CURRENT FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: 09/730,893
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 09/244,675
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: 60/073,629
; PRIOR FILING DATE: 1998-04-02
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-940-173A-1

Query Match 100.0%; Score 6; DB 9; Length 6;

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OM nucleic - nucleic search, using sw model

Run on: July 6, 2003, 08:30:00 ; Search time 65.5714 Seconds
(without alignments)
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Title: US-09-540-843-12

Perfect score: 6
Sequence: 1 ccctaa 6

Scoring table: IDENTITY_NUC

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Searched: 1085931 seqs, 780495707 residues

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Post-processing: Minimum Match 0%

Maximum Match 100%

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- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
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- 9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
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c 2	6	100.0	6	9	US-10-122-630-12
c 3	6	100.0	6	9	US-10-122-633-11
c 4	6	100.0	6	9	US-10-122-633-12
c 5	6	100.0	6	9	US-09-940-173A-1
c 6	6	100.0	6	10	US-09-817-387-29
c 7	6	100.0	6	10	US-09-735-363A-49
c 8	6	100.0	6	10	US-09-730-893-1
c 9	6	100.0	7	9	US-09-940-173A-6
c 10	6	100.0	7	10	US-09-730-893-6
c 11	6	100.0	8	9	US-09-940-173A-4
c 12	6	100.0	8	10	US-09-730-893-4
c 13	6	100.0	9	10	US-09-728-574-19
c 14	6	100.0	10	9	US-10-044-692-294
c 15	6	100.0	10	9	US-10-044-539-294
c 16	6	100.0	10	12	US-10-033-145-56
c 17	6	100.0	10	12	US-10-033-145-358
c 18	6	100.0	10	12	US-10-033-145-613
c 19	6	100.0	10	12	US-10-033-145-1694

c 20	6	100.0	11	9	US-09-835-370-63	Sequence 63, Appl
c 21	6	100.0	11	9	US-10-122-630-5	Sequence 5, Appl
c 22	6	100.0	11	9	US-10-122-630-9	Sequence 9, Appl
c 23	6	100.0	11	9	US-10-122-633-5	Sequence 5, Appl
c 24	6	100.0	11	9	US-10-122-633-9	Sequence 9, Appl
c 25	6	100.0	11	9	US-09-249-155-57	Sequence 57, Appl
c 26	6	100.0	11	9	US-09-942-310-7	Sequence 7, Appl
c 27	6	100.0	11	9	US-09-942-310-44	Sequence 44, Appl
c 28	6	100.0	11	9	US-10-038-335-9	Sequence 9, Appl
c 29	6	100.0	11	10	US-09-057-351-2	Sequence 2, Appl
c 30	6	100.0	12	8	US-08-463-404-2	Sequence 2, Appl
c 31	6	100.0	12	8	US-08-463-404-3	Sequence 3, Appl
c 32	6	100.0	12	8	US-08-463-404-7	Sequence 7, Appl
c 33	6	100.0	12	9	US-10-132-002-1	Sequence 1, Appl
c 34	6	100.0	12	9	US-10-132-002-3	Sequence 3, Appl
c 35	6	100.0	12	9	US-10-073-118-18	Sequence 18, Appl
c 36	6	100.0	12	9	US-10-117-108A-41	Sequence 41, Appl
c 37	6	100.0	12	9	US-10-117-108A-53	Sequence 53, Appl
c 38	6	100.0	12	9	US-09-984-664-11	Sequence 11, Appl
c 39	6	100.0	12	10	US-09-057-351-39	Sequence 39, Appl
c 40	6	100.0	12	10	US-09-968-355-1	Sequence 1, Appl
c 41	6	100.0	12	10	US-09-375-924C-6	Sequence 6, Appl
c 42	6	100.0	13	9	US-09-893-252-4	Sequence 4, Appl
c 43	6	100.0	13	9	US-10-038-335-1	Sequence 1, Appl
c 44	6	100.0	13	9	US-10-038-335-2	Sequence 2, Appl
c 45	6	100.0	14	8	US-08-591-486B-123	Sequence 123, App

ALIGNMENTS

RESULT 1
US-10-122-630-11/c
; Sequence 11, Application US/10122630
; Publication No. US20030032610A1
; GENERAL INFORMATION:
; APPLICANT: Glitchrest, Barbara A.
; APPLICANT: Eller, Mark S.
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using
; TITLE OF INVENTION: Oligonucleotides
; FILE REFERENCE: 0054.1088-018
; CURRENT APPLICATION NUMBER: US/10/122,630
; CURRENT FILING DATE: 2002-04-12
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/467,012
; PRIOR FILING DATE: 1996-06-03
; PRIOR APPLICATION NUMBER: PCT/US96/08386
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: US 09/540,843
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: PCT/US01/10162
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-630-11

Query Match 100.0%; Score 6; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTAA 6
Db 6 CCCTAA 1

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OM nucleic - nucleic search, using sw model

Run on: July 6, 2003, 07:52:05 ; Search time 31.0714 seconds
(without alignments)
59.220 Million cell updates/sec

Title: US-09-540-843-12

Perfect score: 6

Sequence: 1 ccctaa 6

Scoring table: IDENTITY_NUC

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Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 558892

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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- 6: /cgn2.6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	6	100.0	6	1	US-08-381-097A-3
C 2	6	100.0	6	1	US-08-381-097A-5
C 3	6	100.0	6	1	US-08-153-051B-4
C 4	6	100.0	6	1	US-08-337-684-2
C 5	6	100.0	6	2	US-08-151-477A-4
C 6	6	100.0	6	2	US-08-670-999-3
C 7	6	100.0	6	3	US-08-729-598-4
C 8	6	100.0	6	3	US-08-819-867-9
C 9	6	100.0	6	3	US-08-819-867-27
C 10	6	100.0	6	3	US-08-630-019A-1
C 11	6	100.0	6	3	US-09-018-545-3
C 12	6	100.0	6	4	US-09-114-399-3
C 13	6	100.0	6	5	PT-US96-01206-1
C 14	6	100.0	7	3	US-08-729-598-8
C 15	6	100.0	8	3	US-08-838-545-15
C 16	6	100.0	8	3	US-08-838-545-30
C 17	6	100.0	8	3	US-08-838-545-34
C 18	6	100.0	8	4	US-09-349-532-15
C 19	6	100.0	8	4	US-09-349-532-30
C 20	6	100.0	8	4	US-09-349-532-34
C 21	6	100.0	9	1	US-08-337-684-3
C 22	6	100.0	9	3	US-08-630-019A-27
C 23	6	100.0	9	3	US-09-069-434-14
C 24	6	100.0	9	3	US-08-838-545-16
C 25	6	100.0	9	4	US-09-349-532-16
C 26	6	100.0	10	1	US-08-192-300-18
C 27	6	100.0	10	2	US-08-531-743-10

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Sequence 11, Appli
Sequence 12, Appli
Sequence 36, Appli

ALIGNMENTS

RESULT 1
US-08-381-097A-3/c
; Sequence 3, Application US/08381097A
; Patent No. 5643890
; GENERAL INFORMATION:
; APPLICANT: Iverson, Patrick L.
; TITLE OF INVENTION: Synthetic Oligodeoxyribonucleotides
; TITLE OF INVENTION: Which Mimic Telomeric Sequences for Use in the Treatment
; TITLE OF INVENTION: of Cancer and Other Diseases
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zarely, McKee, Thomte, Voorhees, & Sease
; STREET: 801 Grand Suite 3200
; CITY: Des Moines
; STATE: Iowa
; COUNTRY: United States
; ZIP: 50309
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/381,097A
; FILING DATE: 31-JAN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Nebel, Heidi S
; REGISTRATION NUMBER: 37,719
; REFERENCE/DOCKET NUMBER: unmc 63092
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 515-288-3667
; TELEFAX: 515-288-1338
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-381-097A-3

Query Match 100.0%; Score 6; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.8e+07;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CCCTAA 6

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Db          6 CCCTAA 1
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RESULT 2
US-08-381-097A-5
; Sequence 5, Application US/08381097A
; Patent No. 5643890
; GENERAL INFORMATION:
; APPLICANT: Iverson, Patrick L.
; APPLICANT: Mata, John E.
; TITLE OF INVENTION: Synthetic Oligodeoxyribonucleotides
; TITLE OF INVENTION: Which Mimic Telomeric Sequences for Use in the Treatment
; TITLE OF INVENTION: of Cancer and Other Diseases
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zarely, McKee, Thomte, Voorhees, & Sease
; STREET: 801 Grand Suite 3200
; CITY: Des Moines
; STATE: Iowa
; COUNTRY: United States
; ZIP: 50309
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/381,097A
; FILING DATE: 31-JAN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Nebel, Heidi S
; REGISTRATION NUMBER: 37,719
; REFERENCE/DOCKET NUMBER: ummc 63092
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 515-288-3667
; TELEFAX: 515-288-1338
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-381-097A-5

Query Match          100.0%; Score 6; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.8e+07;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 CCCTAA 6
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Db          1 CCCTAA 6

RESULT 3
US-08-153-051B-4
; Sequence 4, Application US/08153051B
; Patent No. 5645986
; GENERAL INFORMATION:
; APPLICANT: Michael D. West
; APPLICANT: Jerry W. Shay
; APPLICANT: Woodring E. Wright
; APPLICANT: Elizabeth Blackburn
; APPLICANT: Nam Woo Kim
; APPLICANT: Calvin B. Harley
; APPLICANT: Scott L. Weinrich
; APPLICANT: Catherine Strahl
; APPLICANT: Michael J. McEachern
; APPLICANT: Homayoun Vaziri

Query Match          100.0%; Score 6; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.8e+07;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 CCCTAA 6
          |||||
Db          1 CCCTAA 6

RESULT 4
US-08-337-684-2/c
; Sequence 2, Application US/08337684
; Patent No. 5686306
; GENERAL INFORMATION:
; APPLICANT: West, Michael David
; APPLICANT: Shay, Jerry
; APPLICANT: Wright, Woodring E.
; TITLE OF INVENTION: METHODS AND REAGENTS FOR
; TITLE OF INVENTION: MEASURING TELOMERES
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
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SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/337,684
FILING DATE: No. 5686306ember 10, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/151,477
FILING DATE: No. 5686306ember 12, 1993
APPLICATION NUMBER: 08/153,051
FILING DATE: No. 5686306ember 12, 1993
APPLICATION NUMBER: 08/060,952
FILING DATE: May 13, 1993
APPLICATION NUMBER: 08/038,766
FILING DATE: March 24, 1993
APPLICATION NUMBER: 07/882,438
FILING DATE: May 13, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 210/085
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-337-684-2

Query Match 100.0%; Score 6; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. NO. 4.8e+07;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTAA 6
Db 6 CCCTAA 1

RESULT 5
US-08-151-477A-4
Sequence 4, Application US/08151477A
Patent No. 5830644
GENERAL INFORMATION:
APPLICANT: Michael D. West
APPLICANT: Jerry W. Shay
APPLICANT: Woodring E. Wright
APPLICANT: Elizabeth Blackburn
APPLICANT: Nam Woo Kim
APPLICANT: Calvin B. Harley
APPLICANT: Scott L. Weinrich
APPLICANT: Catherine Strahl
APPLICANT: Michael J. McEachern
APPLICANT: Homayoun Vaziri
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
TITLE OF INVENTION: CONDITIONS RELATED TO TELFOMERE
TITLE OF INVENTION: LENGTH AND/OR TELOMERASE ACTIVITY
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/151,477A
FILING DATE: No. 5830644ember 12, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/038,766
FILING DATE: March 24, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 202/189
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 6
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-151-477A-4
Query Match 100.0%; Score 6; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. NO. 4.8e+07;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTAA 6
Db 1 CCCTAA 6

RESULT 6
US-08-670-999-3/C
Sequence 3, Application US/08670999
Patent No. 5849727
GENERAL INFORMATION:
APPLICANT: Porter, Thomas R.
APPLICANT: Iverson, Patrick L.
TITLE OF INVENTION: Compositions and Methods for Altering
TITLE OF INVENTION: the Biodistribution of Biological Agents
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zarley, McKee, Thomte, Voorhees & Sease
STREET: 801 Grand Suite 3200
CITY: Des Moines
STATE: Iowa
COUNTRY: United States
ZIP: 50309
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/670,999
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Nebel, Heidi S. 37,719
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: unmc 107A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 515-288-3667
TELEFAX: 515-288-1338
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO

; ANTI-SENSE: YES
US-08-670-999-3

Query Match 100.0%; Score 6; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.8e+07;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTAA 6
|||||
Db 6 CCCTAA 1

RESULT 7

US-08-729-598-4/c
; Sequence 4, Application US/08729598

; Patent No. 6001657

; GENERAL INFORMATION:

; APPLICANT: Hardin, Charles C.

; APPLICANT: Brown II, Bernard A.

; APPLICANT: Roberts, John J.

; APPLICANT: Pelsue, Stephen A.

; TITLE OF INVENTION: Antibodies That Selectively Bind

; TITLE OF INVENTION: Quadruplex Nucleic Acids

; NUMBER OF SEQUENCES: 13

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Sorjini J. Biswas

; STREET: P.O. Box 37428

; CITY: Raleigh

; STATE: No. 6001657th Carolina

; COUNTRY: USA

; ZIP: 27627

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; APPLICATION NUMBER: US/08/729,598

; FILING DATE: 11-OCT-1996

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: Biswas, Sorjini J.

; REGISTRATION NUMBER: 39,111

; REFERENCE/DOCKET NUMBER: 5051-301A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (919) 854-1400

; TELEFAX: (919) 854-1401

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 6 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: not relevant

; MOLECULE TYPE: DNA (genomic)

US-08-729-598-4

Query Match 100.0%; Score 6; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.8e+07;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTAA 6
|||||
Db 6 CCCTAA 1

RESULT 8

US-08-819-867-9/c

; Sequence 9, Application US/08819867

; Patent No. 6007989

; GENERAL INFORMATION:

; APPLICANT: Michael D. West

; APPLICANT: Calvin B. Harley

; APPLICANT: Scott L. Weinrich

; APPLICANT: Catherine M. Strahl
; APPLICANT: Michael J. Mceachern
; APPLICANT: Jerry Shay
; APPLICANT: Woodring E. Wright
; APPLICANT: Elizabeth H. Blackburn
; APPLICANT: Nam Woo Kim
; APPLICANT: Homayoun Vaziri
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
; TITLE OF INVENTION: CONDITIONS RELATED TO
; TITLE OF INVENTION: TELOMERE LENGTH AND/OR
; TITLE OF INVENTION: TELOMERASE ACTIVITY
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/819,867
; FILING DATE: March 14, 1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/153,051
; FILING DATE: No. 6007989ember 12, 1993
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Chambers, Daniel M.
; REGISTRATION NUMBER: 34,561
; REFERENCE/DOCKET NUMBER: 224/232
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-819-867-9

Query Match 100.0%; Score 6; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.8e+07;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTAA 6
|||||
Db 6 CCCTAA 1

RESULT 9

US-08-819-867-27

; Sequence 27, Application US/08819867

; Patent No. 6007989

; GENERAL INFORMATION:

; APPLICANT: Michael D. West

; APPLICANT: Calvin B. Harley

; APPLICANT: Scott L. Weinrich

; APPLICANT: Catherine M. Strahl

; APPLICANT: Michael J. Mceachern

; APPLICANT: Jerry Shay

; APPLICANT: Woodring E. Wright

; APPLICANT: Elizabeth H. Blackburn

APPLICANT: Nam Woo Kim
APPLICANT: Homayoun Vaziri
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
TITLE OF INVENTION: CONDITIONS RELATED TO
TITLE OF INVENTION: TELOMERE LENGTH AND/OR
TITLE OF INVENTION: TELOMERASE ACTIVITY
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,867
FILING DATE: March 14, 1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/153,051
FILING DATE: No. 6007989ember 12, 1993
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Chambers, Daniel M.
REGISTRATION NUMBER: 34,561
REFERENCE/DOCKET NUMBER: 224/232
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-819-867-27

Query Match 100.0%; Score 6; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.8e+07;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTAA 6
Db 1 CCCTAA 6

RESULT 10
US-08-630-019A-1/c
Sequence 1, Application US/08630019A
Patent No. 6015710
GENERAL INFORMATION:
APPLICANT: Shay, Jerry W.
APPLICANT: Wright, Woodring E.
APPLICANT: Piatyszek, Mieczyslaw A.
APPLICANT: Corey, David
APPLICANT: No. 6015710ton, James C.
TITLE OF INVENTION: Modulation of Mammalian Telomerase by
TITLE OF INVENTION: Peptide Nucleic Acids
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California

COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,019A
FILING DATE: 09-JUN-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-0016000US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "peptide nucleic acid (PNA),
DESCRIPTION: where (deoxy)ribose-phosphate linkages are replaced by
DESCRIPTION: N-(2-aminoethyl)glycine units linked to nucleotide bases via
DESCRIPTION: glycine amino nitrogen through a methylenecarbonyl linker"
US-08-630-019A-1

Query Match 100.0%; Score 6; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.8e+07;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTAA 6
Db 6 CCCTAA 1

RESULT 11
US-09-018-545-3/c
Sequence 3, Application US/09018545
Patent No. 6087493
GENERAL INFORMATION:
APPLICANT: Wheelhouse, Richard T.
APPLICANT: Hurley, Laurence H.
TITLE OF INVENTION: PORPHYRIN COMPOUNDS AS TELOMERASE
TITLE OF INVENTION: INHIBITORS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: U.S.
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/018,545
FILING DATE: Concurrently Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/037,295
FILING DATE: 05-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: UTSB:654

TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-018-545-3

Query Match 100.0%; Score 6; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.8e+07;
Matches 6; Conservative 0; Mismatches 0; Indels 0;

Qy 1 CCCTAA 6
Db 6 CCCTAA 1

RESULT 12
US-09-114-399-3/c
Sequence 3, Application US/09114399
Patent No. 6245747

GENERAL INFORMATION:
APPLICANT: Porter, Thomas R.
APPLICANT: Iversen, Patrick L.
APPLICANT: Meyer, Gary D.
TITLE OF INVENTION: Targeted Site Specific Drug Delivery
TITLE OF INVENTION: Compositions and Method of Use
FILE REFERENCE: 0450-0310.31
CURRENT APPLICATION NUMBER: US/09/114,399
CURRENT FILING DATE: 1998-07-13
PRIOR APPLICATION NUMBER: US 08/615,495
PRIOR FILING DATE: 1996-03-12
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 6
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: PS-ODN
US-09-114-399-3

Query Match 100.0%; Score 6; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.8e+07;
Matches 6; Conservative 0; Mismatches 0; Indels 0;

Qy 1 CCCTAA 6
Db 6 CCCTAA 1

RESULT 13
PCT-US96-01206-1/c
Sequence 1, Application PC/TUS9601206
GENERAL INFORMATION:
APPLICANT: Iverson, Patrick L.
APPLICANT: Mata, John E.
TITLE OF INVENTION: Synthetic Oligodeoxynucleotides Which
Mimic Telomeric Sequences for Use in the Treatment of
Cancer and Other Diseases
TITLE OF INVENTION: Cancer and Other Diseases
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zarley, McKee, Thomte, Voorhees & Sease
STREET: 801 Grand Avenue Suite 3200
CITY: Des Moines
STATE: Iowa
COUNTRY: United States
ZIP: 50309
COMPUTER READABLE FORM: disk
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/01206
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/381,097
FILING DATE: 31-JAN-1995
ATTORNEY/AGENT INFORMATION:

NAME: Nebel, Heidi S.
REGISTRATION NUMBER: 37,719
REFERENCE/DOCKET NUMBER: UNMC# 63092
TELECOMMUNICATION INFORMATION:

TELEPHONE: 515-288-3667
TELEFAX: 515-288-1338
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: YES
PCT-US96-01206-1

Query Match 100.0%; Score 6; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.8e+07;
Matches 6; Conservative 0; Mismatches 0; Indels 0;

Qy 1 CCCTAA 6
Db 6 CCCTAA 1

RESULT 14
US-08-729-598-8/c
Sequence 8, Application US/08729598
Patent No. 6001657
GENERAL INFORMATION:
APPLICANT: Hardin, Charles C.
APPLICANT: Brown II, Bernard A.
APPLICANT: Roberts, John J.
APPLICANT: Pelsue, Stephen A.
TITLE OF INVENTION: Antibodies That Selectively Bind
Quadruplex Nucleic Acids
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sorojini J. Biswas
STREET: P.O. Box 37428
CITY: Raleigh
STATE: No. 6001657th Carolina
COUNTRY: USA
ZIP: 27627

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/729,598
FILING DATE: 11-OCT-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Biswas, Sorojini J.
REGISTRATION NUMBER: 39,111
REFERENCE/DOCKET NUMBER: 5051-301A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 854-1400
TELEFAX: (919) 854-1401
INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 7 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: DNA (genomic)
US-08-729-598-8

Query Match 100.0%; Score 6; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. NO. 4.1e+07;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCCTAA 6
Db 7 CCCTAA 2

RESULT 15

US-08-838-545-15/c
; Sequence 15, Application US/08838545
; Patent No. 6046307
; GENERAL INFORMATION:
; APPLICANT: Shay, Jerry W.
; APPLICANT: Wright, Woodring E.
; APPLICANT: Piatyszek, Mieczyslaw A.
; APPLICANT: Corey, David R.
; APPLICANT: No. 6046307ton, James C.
; TITLE OF INVENTION: Modulation of Mammalian Telomerase by
; TITLE OF INVENTION: Peptide Nucleic Acids
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,545
; FILING DATE: 09-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,019
; FILING DATE: 09-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-001610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "peptide nucleic acid (PNA),
; DESCRIPTION: where (deoxy(ribose-phosphate linkages are replaced by
; DESCRIPTION: N-(2-aminoethyl)glycine units linked to nucleotide bases via
; DESCRIPTION: glycine amino N through a methylenecarbonyl linker"
US-08-838-545-15

Query Match 100.0%; Score 6; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. NO. 3.6e+07;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCCTAA 6
Db 7 CCCTAA 2

Search completed: July 6, 2003, 09:42:21
Job time : 32.0714 secs

